BioMate 5 User Manual

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Issue 1
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Thermo Spectronic (Europe, Middle East and Africa)
Mercers Row, Cambridge CB5 8HY, UK
Tel: +44 (0)1223 446600
Fax: +44 (0)1223 446644
E-mail: info@thermospectronic.co.uk
www.thermospectronic.com

Thermo Spectronic (North America and Latin America)
820 Linden Avenue, Rochester, NY 14625, USA
Tel: (800) 654-9955 or (716) 248-4000
Fax: (716) 248-4014
E-mail:info@thermospectronic.com
www.thermospectronic.com

For Indian Sub-continent, Far East and Australasia
Contact Thermo Spectronic (Europe, Middle East and Africa)

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USER MANUAL

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Environmental and Electrical Requirements

Your BioMate 5 spectrophotometer has been designed to operate under the environmental and electrical requirements listed below.

Line Voltages 100-240V ±10% (max)
50-60Hz ±10%

Power input 180VA

Operating Environment

Temperature	5°C to 40°C
Rate of change of temperature	<1°C/hour
Relative humidity	20% to 90% non condensing
Absolute humidity	3g/m^3 to 20g/m^3
Air pressure	68kPa to 106kPa
Air velocity	0.5m/s

Transport and storage requirements

Temperature	-20°C to 70°C
Rate of change of temperature	5°C/hour
Relative humidity	5% to 95% non condensing
Absolute humidity	0.1g/m^3 to 35g/m^3
Air pressure	25kPa to 110kPa
Air velocity	< 30m/s

For Indoor Use only.

Installation Category II.

The following are important for the safe operation of the instrument:

When connecting the instrument into a mains socket, ensure the socket is earthed. Position the instrument sufficiently away from other objects, walls etc, to ensure a free airflow around the instrument and also to allow access to the mains switch on the rear of the product.

The mains switch is marked “0” and “I”. When “0” is depressed the instrument is off. When “I” is depressed, the instrument is switched on.

The fuse on the internal power supply is rated at 3.15A (type T).

The following connectors are provided on the rear of the instrument:

Sipper: Use to connect a SuperSipper or MiniSipper
RS232: Use to connect a computer or printer with an RS232 interface
Parallel: Use to connect a printer with a parallel interface
Rec.: Use to connect a Chart Recorder

Ensure that any equipment such as printers which are connected to the sockets on the rear panel conform to relevant IEC safety standards.

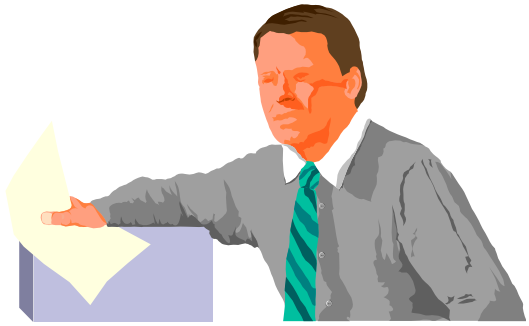
Trademarks

All company, product, or brand names are trademarks or registered trademarks of their respective holders.

THIS SYSTEM IS DESIGNED TO BE USER INSTALLED -

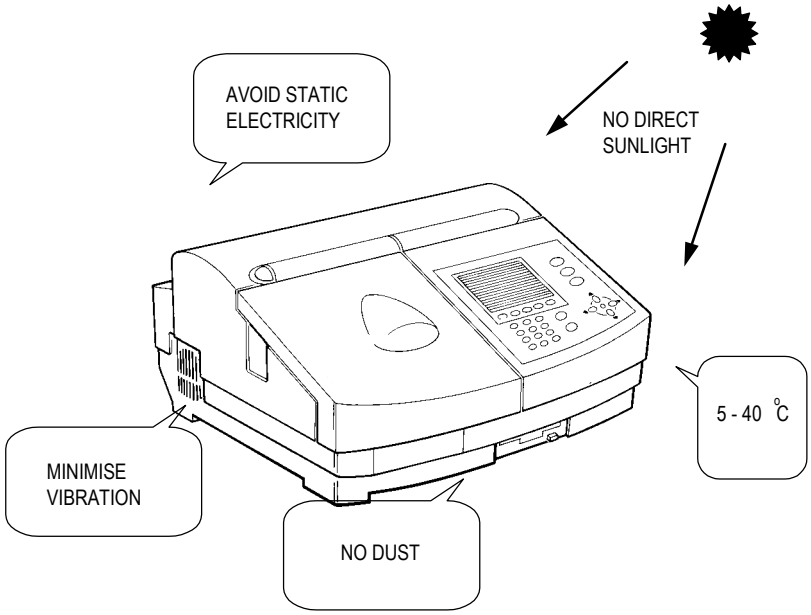
So, use the following procedures to quickly get your new spectrophotometer system in position and running the way you want it.

1. Read the Safety instructions on page 5 of this manual.

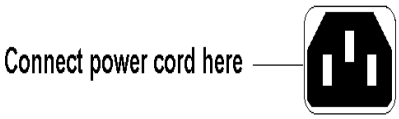


2. Check the component parts of the system against the Despatch Note and Packing List. **Immediately report any discrepancies by telephone, and then confirm in writing**.

3. Find a suitable location (see below).

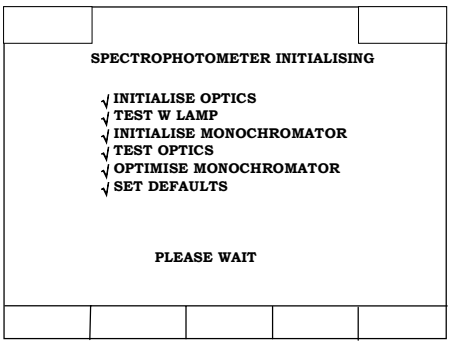


4. Connect the supplied power cord to the spectrophotometer.



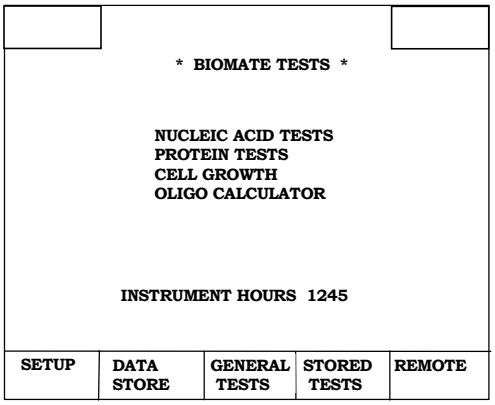
5. Ensure NO SAMPLE(S) are in place in the sample compartment .
- Turn the spectrophotometer on.

6. The Local Control display shows this initialisation sequence. Successive items are ticked as the initalisation proceeds.



Approximately
3 minutes

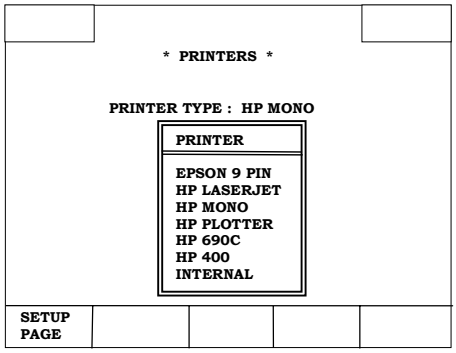
7. After initialisation, the BioMate Tests Home Page is displayed:



THIS COMPLETES THE INSTALLATION OF A STANDALONE SYSTEM

Connecting an External Printer

- **ENSURE THAT THE SPECTROPHOTOMETER IS TURNED OFF**
- Connect the printer to the Parallel port on the spectrophotometer using the cable supplied.
- POWER UP THE SYSTEM AND ALLOW TO INITIALISE.
- From HOME page, press SETUP.
- Select PRINTER using the cursor keys.
- Press ENTER. The PRINTERS page is displayed with the default printer (HP Mono / Internal) selected.



- Press ENTER again to display the Printer Menu and, using the cursor keys, select the required printer.
- Press ENTER.

SAFETY

- THIS SPECTROPHOTOMETER SYSTEM HAS BEEN DESIGNED TO BE USER INSTALLED.

  READ THIS PAGE CAREFULLY BEFORE INSTALLING AND USING THE INSTRUMENT AND ITS ACCESSORIES.

- The safety statements in this manual comply with the requirements of the HEALTH AND SAFETY AT WORK ACT 1974.

- The instrument and accessories described in this manual are designed to be used by properly trained personnel only. Adjustment, maintenance and repair of exposed equipment must be carried out only by qualified personnel who are aware of the hazards involved. Where indicated in the relevant manual, certain maintenance processes may be carried out by the user, who must be fully aware of, and apply, the following safety precautions.

- For the correct and safe use of this instrument and its accessories it is essential that both operating and servicing personnel follow generally accepted safety procedures in addition to the safety precautions specified in this manual.

- Specific warning and caution statements, where applicable, can be found throughout the manual. Warning and caution statements and/or symbols are marked on the apparatus where necessary.

- The instrument covers and accessories should only be removed by personnel who have been trained to avoid the risk of electric shocks. The mains electricity supply to the instrument must be disconnected at the mains supply connector and at least three minutes allowed for capacitors to discharge.

- Some of the chemicals used in spectrophotometry are corrosive, and/or flammable and samples may be radioactive, toxic or potentially infective. Care should be taken to follow the normal laboratory procedures for handling chemicals.

- The UV radiation from a deuterium lamp can be harmful to the skin and eyes. Always view the lamp through protective glasses/goggles that will absorb the UV radiation and avoid looking directly at the deuterium arc. Do not expose the skin to direct or reflected UV radiation.

- Whenever it is likely that safety protection has been impaired, the instrument and/or accessory must be made inoperative and secured against any unintended operation. The matter should then be referred to the appropriate servicing authority. Safety protection is likely to be impaired if for example, the instrument fails to perform the intended measurements or shows visible damage.

GENERAL

Introduction

- The range comprises a group of UV-Visible spectrophotometers which can be controlled independently via an integral keypad and LCD display, or externally from a computer.

- The system is composed of a spectrophotometer with integral keypad, LCD display, 1.44 Mbyte Disk Drive, Local Control Software and output device.

LCD display contrast can be controlled during initialisation, or from the BIOMATE TESTS, GENERAL TESTS and SETUP pages using the left and right arrow keys.

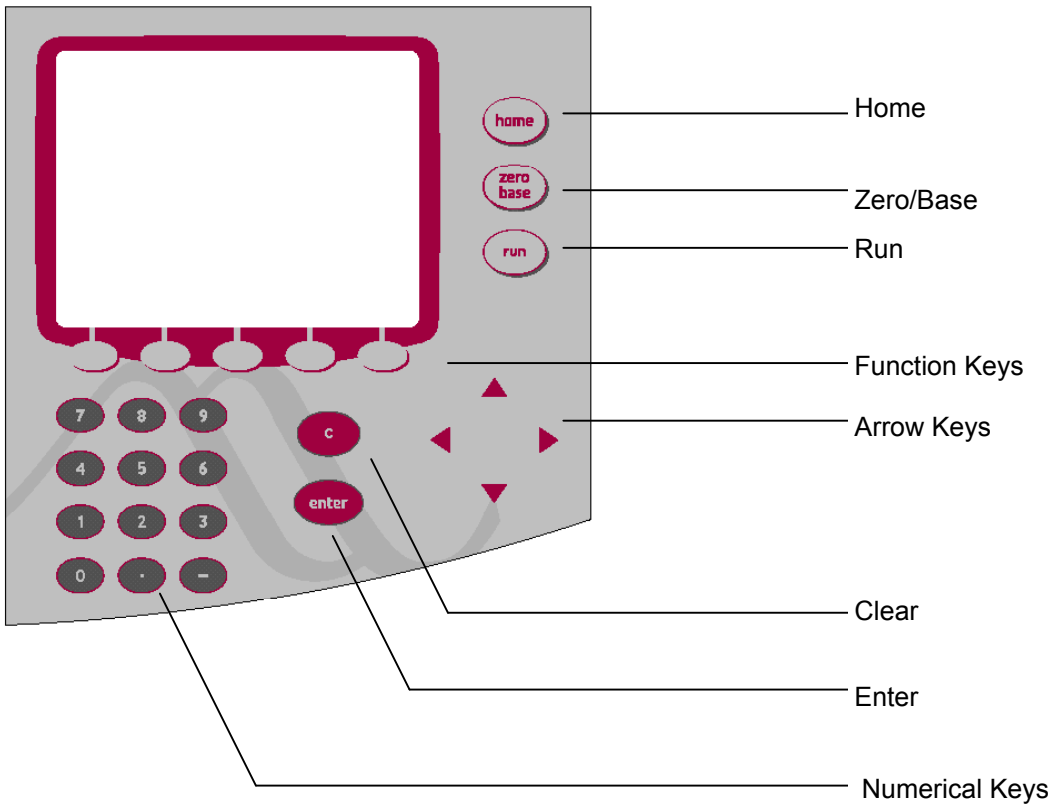
- Always remove disks from the disk drive when not in use. Never power-up the instrument with a disk in place, as permanent damage may be caused to the disk.

The only exception to this rule is when upgrading the instrument software or installing the UVCalc accessory. Then, automatic recognition of a software disk causes an automatic upgrade of the software.

- The Local Control software controls all aspects of the systems operation.

- Where installed, the UVCalc software accessory provides automatic calculation of results from measurements using user-defined equations in SCAN, FIXED and QUANT modes.

User Interface



Key	Operation
Arrow Keys	Highlight menu options, move track cursor, or move 7 Cell Changer, depending on page in use. Change display contrast with <> from Home Page.
Numerical Keys	Enter numbers, minus and decimal point.
Function Keys	Access and perform system functions. Operation depends on screen in use, and is indicated by labels at bottom of screen.
Clear	Clears entry leaving field or parameter ready for new entry, clears pop-up, and clears error messages.
Enter	Enters changes to field or parameter.
Run	Starts instrument measurement according to current method.
Home	Returns to Home page.
Zero/Base	Performs a zero or baseline as appropriate to application. **REMOVE THE SAMPLE AND ENSURE THAT BOTH SAMPLE AND REFERENCE BEAMS ARE CLEAR OR CONTAIN THE BASELINE SAMPLES RELEVANT TO THE ANALYSIS BEFORE ZEROING THE INSTRUMENT OR PERFORMING A BASELINE SCAN.**

Parameter entry

The BioMate 5 has the following types of parameter entries:

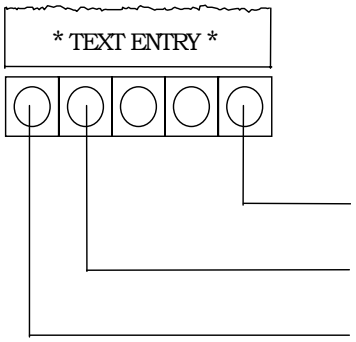
- **Pop-up editors** are provided for entering numerical parameters. The valid range for the parameter is displayed in the pop-up window. Enter a new value using the numeric keypad and then press ENTER to accept the change. Press CLEAR to return to the previous screen without changing the parameter.

- **Toggle entries** offer two options for a parameter. Press ENTER to switch between the two options, then press the up or down arrow key to move to another parameter.

- **Pop-up lists** show multiple options for a parameter or display messages. Press the Up or Down Arrow key to highlight the required value, then press ENTER to select it.

- **Graphical cursor selections** are used in graphical displays. The cursor appears as a vertical line. Use the Arrow keys to move the cursor to the required position on the graph and then press ENTER to select it.

- **Text entry screens** are provided for alphanumeric parameter input. Use the Arrow keys to move the cursor to the required character in the list and press ENTER. Numbers are entered using the numeric keypad. If you make a mistake, CLEAR will remove the whole entry.



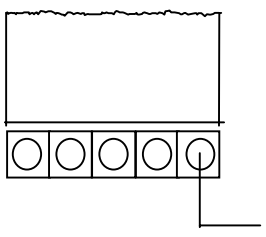
(←) - Acts as backspace and clears the last character in the entered text.

ACCEPT - Enters the names and returns to the calling screen.

CANCEL - Abandons the naming operation and returns the calling screen. The original entry is not changed.

Local and Computer Control

- From switch-on a standalone instrument will automatically be under Local Control. To enable control from an external computer via the RS232C port, first ensure the instrument is idle and then press REMOTE on the BioMate Tests or General Tests pages.



REMOTE

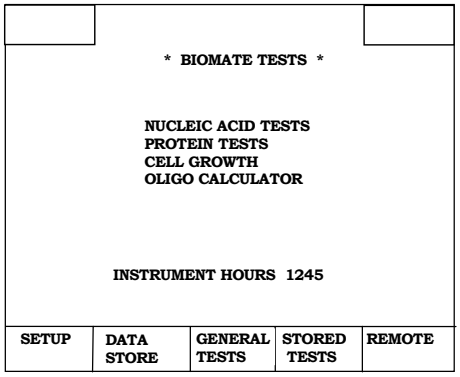
- To return to Local Control, first ensure the instrument is idle and then relinquish control of the communications port by the PC software. Press the HOME key on the instrument. The BioMate Tests page will be redisplayed, and the spectrophotometer may now be controlled via the keypad.

BioMate and General Tests

BioMate 5 provides an assortment of specific tests used to characterize biological and biochemical substances. These tests fall into the following categories :

- Nucleic acid measurements
- Protein measurements
- Cell growth analysis
- Oligonucleotide calculations

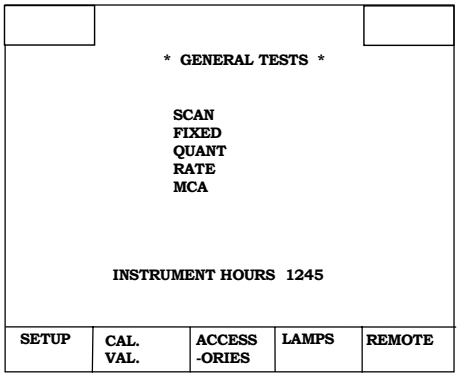
These tests are accessed from the BioMate Tests page, which is the default Home Page:



In addition, BioMate 5 also provides a range of more general operating modes:

- Scan
- Fixed
- Quantification
- Rate
- MCA (Multi Component Analysis)

These applications are accessed via the GENERAL TESTS function key on the default BioMate Tests page:



SmartStart feature

- BioMate's SmartStart feature enables you to select the test methods you use most frequently and have them appear when you start up your instrument.

Setting up SmartStart

- Press the **STORED TESTS** function key on the BIOMATE TESTS page. A list of all the tests on the instrument appears on the screen.
- Move the cursor to the required tests and press the **SMART START** function key. A tick will appear at the left of each selected test. This set of tests will now be listed on the new Home page.
- To remove any of these tests from the SmartStart Home page listing, navigate to the Stored Tests page, move the cursor to the required test and press **SMART START** again.

BIOMATE APPLICATIONS

All of the parameters for the BioMate applications described in this section are factory-set. This means that if you want to change the parameters, you will need to specify a different name to save the new test parameters. Appendix A lists all the parameters used in each pre-set test. Appendix B lists the calculations used by each test.

Nucleic acid measurements

You can use these tests to determine the concentration and purity of nucleic acid in a given sample.

- **DNA** – measures absorbance at 260 and 280nm or at 260 and 230nm; determines concentration and purity based on absorbance ratio and absorbance difference.
- **DNA with scan** – records absorbance scan between 260 and 280nm or between 260 and 230nm; determines concentration and purity based on absorbance ratio and absorbance difference.
- **dsDNA** – measures absorbance at 260nm; calculates concentration based on absorbance and concentration factor.
- **ssDNA, RNA** – measures absorbance at 260nm; calculates concentration based on absorbance and concentration factor.
- **Oligonucleotides** – measures absorbance at 260nm; calculates concentration based on absorbance and concentration factor or calculates concentration based on absorbance and concentration factor determined by the oligo calculator application.

Several of these categories include multiple tests that are similar, so the individual sections do not include screen shots for each test. For example, the parameters are the same for the Direct UV measurement of dsDNA and RNA tests, but the factor used to convert absorbance to concentration is different. Similarly, for the Direct UV measurement of oligonucleotides tests, the parameters are also the same, but the factors used to convert absorbance to concentration are different. For a complete list of all parameters and calculations for each test, refer to the appendices.

DNA measurement

The DNA measurement group includes two tests that function almost identically – the only difference is in the wavelengths used for the measurements. One test measures absorbance at 260 and 280nm, while the other measures absorbance at 260 and 230nm.

Test parameters

To set test parameters, move the cursor to the appropriate parameter and press **ENTER**.

Note: The following screens show the parameters for the DNA (260/280) test. For the DNA (260/230) test, Wavelength 2 is set to 230nm.

	DNA			
TEST NAME				**DNA (260/280)**
WAVELENGTH 1				**260.0nm**
WAVELENGTH 2				**280.0nm**
REF. WAVELENGTH CORRECTION				**ON**
REF. WAVELENGTH				**320nm**
DNA FACTOR (λ1)				**62.90**
DNA FACTOR (λ2)				**36.00**
DISPLAY PROTEIN				**ON**
PROTEIN FACTOR (λ1)				**757.3**
PROTEIN FACTOR (λ2)				**1552**
DILUTION MULTIPLIER				**1.00**
UNITS				**µg/ml**
SAMPLE POSITIONER				**AUTO 6 + REF**
NUMBER OF SAMPLES				**1**
ID# (0-OFF)				**0**
AUTOPRINT				**OFF**
	PRINT TEST	**SAVE TEST**	**STORED TESTS**	**VIEW RESULTS**

Running DNA measurements

- With the appropriate DNA parameter screen displayed, select the required Sample Positioner mode, number of samples (if appropriate), and initial sample number (ID#).

- Place the blank in the correct cell position.

Note: If you are using the 7 Cell Changer in AUTO 6 + REF mode, place the blank and unknowns in the correct cell positions and press **RUN**. The instrument will measure the blank and samples automatically.

- Press **ZERO/BASE** to measure the blank.

- Place the unknown(s) in the correct cell position(s).

- Press **RUN** to start the measurement. The DNA measurement screen appears. When the instrument is finished measuring the absorbance of the sample, it displays the absorbance, DNA ratio and DNA concentration on a screen like the one shown below.

Note: If all the results do not fit on a single screen, press the Down/Up Arrow key to display the next/previous page of results.

TEST NAME: DNA (260/280)

ID#	ABS(λ1) 260.0nm	ABS(λ1) 280.0nm	ABS(REF λ) 320.0nm	
999	0.123	0.456	0.789	
	DNA RATIO	=	1.7	
	DNA CONC	=	1234.5	µg/ml
	PROTEIN CONC	=	1111.1	µg/ml
1	1.234	1.567	1.890	
	DNA RATIO	=	1.6	
	DNA CONC	=	1234.9	µg/ml
	PROTEIN CONC	=	33.8	µg/ml

	PRINT LIST	SAVE DATA	TEST PAGE	CLEAR RESULTS

DNA measurement with scan

The DNA measurement with scan group includes two tests that function almost identically – the only difference is in the wavelengths used for the measurements. One test measures absorbance between 260 and 280nm, while the other measures absorbance between 260 and 230nm.

Test parameters

Note: The following screens show the parameters for the DNA with scan (260/280) test. For the DNA with scan (260/230) test, Wavelength 2 is set to 230nm.

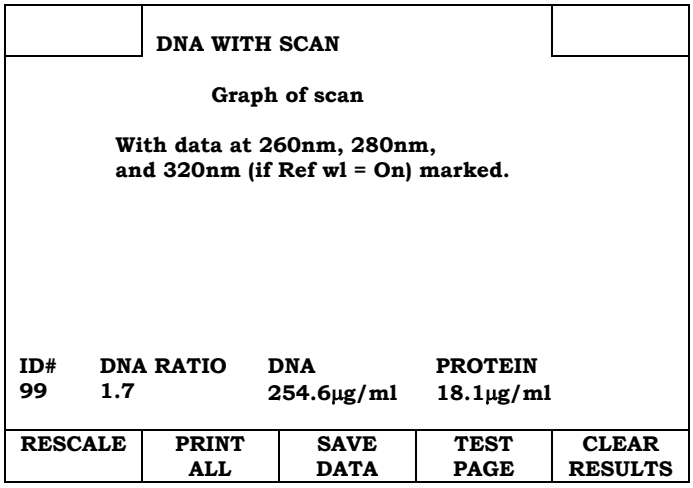
DNA WITH SCAN

TEST NAME	**DNA WITH SCAN**
WAVELENGTH 1	**260.0nm**
WAVELENGTH 2	**280.0nm**
REF. WAVELENGTH CORRECTION	**ON**
REF. WAVELENGTH	**320nm**
DNA FACTOR (λ1)	**62.90**
DNA FACTOR (λ2)	**36.00**
DISPLAY PROTEIN	**YES**
PROTEIN FACTOR (λ1)	**757.3**
PROTEIN FACTOR (λ2)	**1552**
DILUTION MULTIPLIER	**1.00**
UNITS	**µg/ml**
SAMPLE POSITIONER	**AUTO 6 + REF**
NUMBER OF SAMPLES	**1**
ID# (0-OFF)	**0**
AUTOPRINT	**OFF**

SETUP SCAN	**PRINT TEST**	**SAVE TEST**	**STORED TESTS**	**VIEW RESULTS**

Running DNA measurement with scan

- With the appropriate DNA parameter screen displayed, select the required Sample Positioner mode, number of samples (if appropriate), and initial sample number (ID#).
- Place the blank in the correct cell position.
- Press **ZERO/BASE** to measure the blank.
- Place the unknown(s) in the correct cell position(s).
- Press **RUN** to start the measurement.. The DNA measurement screen appears. When the instrument is finished measuring the absorbance scan, it displays a graph of the scan along with the sample ID#, DNA ratio, DNA concentration and protein concentration on a screen like the one shown below.



Direct UV measurements

This group of tests includes:

- dsDNA measurements
- ssDNA and RNA measurements
- Oligonucleotide measurements using an entered factor

These test measurements are set up and run using the same types of test parameters.

Test parameters

Note: The following screens show the parameters for the Direct UV measurement of dsDNA test. For the Direct UV measurement of ssDNA and RNA tests, the parameters are the same, but the factor used to convert absorbance to concentration is 40.
For the Direct UV measurement of oligonucleotides tests, the parameters are also the same, but the factor used to convert absorbance to concentration is 33.

dsDNA

TEST NAME	**dsDNA**
WAVELENGTH	**260.0nm**
FACTOR	**50.00**
DILUTION MULTIPLIER	**1.00**
UNITS	**µg/ml**
SAMPLE POSITIONER	**AUTO 6 + REF**
NUMBER OF SAMPLES	**1**
LOW/HIGH LIMITS	**-9999/9999**
STATISTICS	**OFF**
ID# (0-OFF)	**0**
AUTOPRINT	**OFF**

PRINT TEST | **SAVE TEST** | **STORED TESTS** | **VIEW RESULTS**

Running Direct UV measurements

- With the appropriate Direct UV parameter screen displayed, select the required Sample Positioner mode, number of samples (if appropriate), and initial sample number (ID#).
- Place the blank in the correct cell position.
- Press **ZERO/BASE** to measure the blank.
- Place the unknown(s) in the correct cell position(s).
- Press **RUN** to start the measurement. The Direct UV measurement screen appears. When the instrument is finished measuring the absorbance of the sample, it displays the ID#, absorbance and concentration on a screen like the one shown below.

Note: If all the results do not fit on a single screen, press the Down/Up Arrow key to display the next/previous page of results.

TEST NAME: dsDNA

ID#	ABS 260.0nm	CONC µg/ml	
999	0.121	123.45	LOW
1	0.234	2345.6	
2	0.345	345678	HIGH

	PRINT LIST	SAVE DATA	TEST PAGE	CLEAR RESULTS

Oligonucleotide measurement – calculated factor

The Oligonucleotide measurement using a calculated factor test measures absorbance at 260nm, then converts absorbance to concentration using a factor that the instrument calculates using molecular weight and the extinction coefficient.

Test parameters

OLIGOS (CALC)

TEST NAME	**OLIGOS (CALC)**
WAVELENGTH	**260.0nm**
DILUTION MULTIPLIER	**1.00**
UNITS	**µg/ml, pmol/µl**
SAMPLE POSITIONER	**AUTO 6 + REF**
NUMBER OF SAMPLES	**1**
ID# (0-OFF)	**0**
AUTOPRINT	**OFF**

BASE SEQUENCE =
ATCGTCGATTGAGCATCAGCATGACTAGATCAGAATCGCG

BASE SEQUENCE FACTOR	**26.68**

BASE SEQ.	**PRINT TEST**	**SAVE TEST**	**STORED TESTS**	**VIEW RESULTS**

Running oligonucleotide measurements with a calculated factor

- Enter a base sequence: With the Oligos (calc factor) parameter screen displayed, press BASE SEQ. to view the Base Sequence screen and then follow the instructions in the Oligo calculator functions section of this manual to specify the sequence.
- With the appropriate DNA parameter screen displayed, select the required Sample Positioner mode, number of samples (if appropriate), and initial sample number (ID#).
- Place the blank in the correct cell position.
- Press **ZERO/BASE** to measure the blank.
- Place the unknown(s) in the correct cell position(s).
- Press **RUN** to start the measurement. The Oligos (calc factor) measurement screen appears. When the instrument is finished measuring the absorbance of the sample, it displays the ID#, absorbance and concentration on a screen like the one shown below.

Note: If all the results do not fit on a single screen, press the Down/Up Arrow key to display the next/previous page of results.

TEST NAME: OLIGOS (CALC)

ID#	ABS(λ1) 260.0nm	OLIGOS µg/ml	OLIGOS pmol/µl
999	-0.123	123.4	56.7
1	0.345	12.34	5.67
2	0.678	1.234	0.567
3	1.234	12345	57890

	PRINT LIST	SAVE DATA	TEST PAGE	CLEAR RESULTS

Protein measurements

Bradford (standard & micro), Lowry (standard & micro), BCA (standard & micro) & Biuret measurements

You can use these tests to determine the concentration of protein in a given sample, using the following analytical methods:

- **Bradford** – measures absorbance at 595nm; determines concentration for either standard or micro sample volumes.
- **Lowry** – measures absorbance at 550nm; determines concentration for either standard or micro sample volumes.
- **Bicinchoninic Acid (BCA)** – measures absorbance at 562nm; determines concentration for either standard or micro sample volumes.
- **Biuret** – measures absorbance at 540nm.

Several of these categories include multiple tests that are similar, so this section includes screen shots for the standard Bradford test. For a complete list of all parameters and calculations for each test, refer to Appendices A and B.

Test parameters for preparing and running a standard curve

BRADFORD-STANDARD

TEST NAME	**BRADFORD-STANDARD**
DATE STANDARDS MEASURED	**17/01/01**
WAVELENGTH	**595.0nm**
CURVE FIT	**QUADRATIC**
STANDARDS	**6**
UNITS	**µg/ml**
SAMPLE POSITIONER	**AUTO 6 + REF**
NUMBER OF SAMPLES	**1**
ID# (0-OFF)	**0**
LOW/HIGH LIMITS	**-9999/9999**
STATISTICS	**OFF**
AUTOPRINT	**OFF**

CALIB-RATE	PRINT TEST	SAVE TEST	STORED TESTS	VIEW RESULTS

Preparing and running a standard curve

- With the appropriate protein parameter screen displayed, select **STANDARDS** and press **ENTER**. The STANDARDS screen appears.
- Edit any changed concentration values and then **ACCEPT** the changes.
- When all the parameters are correct, press **CALIBRATE**.
- Place the standards, and blank if required in the correct cell positions as prompted and then follow the on-screen instructions to start the calibration.
- When the instrument has measured all the standards, the CALIBRATION screen will show the absorbance of each standard, along with the equation of the calculated standard curve.

Editing standard curves

You may remeasure any standard on a standard curve. In addition, you may select a different curve fit or delete points from the curve.

To edit a standard

- Press **STANDARDS** on the CALIBRATION screen
- Press **EDIT STD** on the STANDARDS RESULTS screen.
- Select the standard which is to edited by entering its number in the Edit box displayed.
- You may now remove the standard from the calibration, restore a previously ignored value or remeasure the standard's absorbance. Use the Up/Down arrows to select the required option and then follow the on-screen instructions.

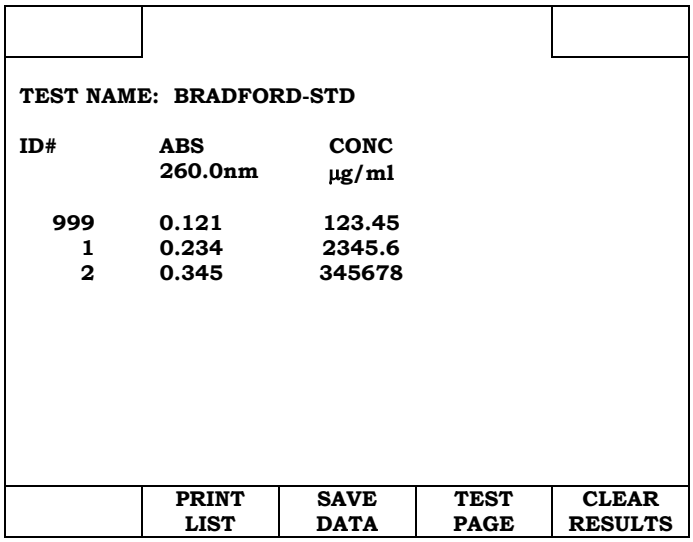
To select a different curve fit for a standard curve

- Press **STANDARDS** on the CALIBRATION screen
- Press **EDIT CURVE** on the STANDARDS RESULTS screen.
- Use the arrow keys to highlight the curve fit you want to use for the standard curve and press **ENTER**. The instrument applies the selected curve fit to the data and displays the new calibration equation and coefficient.

Running protein measurements

- Place the blank in the correct cell position.
- With the appropriate protein parameter screen displayed, press **ZERO/BASE** to measure the blank.
- Place the unknown in the correct cell position.
- Press **RUN**. The protein measurement screen appears and the measurement starts.
- When the instrument is finished measuring the absorbance of the sample, it displays the ID#, absorbance and concentration on a screen like the one shown below.

Note: If all the results do not fit on a single screen, press the Down/Up arrow keys to display the next/previous pages of results.



Direct UV (280, 205)

The Direct UV method determines protein concentration based on absorbance at either 280 or 205nm.

Note: The following screens show the parameters for the Direct UV test at 280nm. For the Direct UV test at 205nm, the Wavelength is set to 205nm.

Test parameters

	DIRECT UV			
TEST NAME				**DIRECT UV (280)**
WAVELENGTH				**280.0nm**
FACTOR				**1.000**
DILUTION MULTIPLIER				**1.00**
UNITS				**mg/ml**
SAMPLE POSITIONER				**AUTO 6 + REF**
NUMBER OF SAMPLES				**1**
ID# (0-OFF)				**0**
LOW/HIGH LIMITS				**-9999/9999**
STATISTICS				**OFF**
AUTOPRINT				**OFF**
	PRINT TEST	**SAVE TEST**	**STORED TESTS**	**VIEW RESULTS**

Running Direct UV measurements

- With the appropriate Direct UV parameter screen displayed, select the required Sample Positioner mode, number of samples (if appropriate), and initial sample number (ID#).
- Place the blank in the correct cell position.
- Press **ZERO/BASE** to measure the blank.
- Place the unknown(s) in the correct cell position(s).
- Press **RUN**. The Direct UV measurement screen appears.
- When the instrument has finished measuring the absorbance of the sample, it displays the ID#, absorbance and concentration on a screen like the one shown below.

TEST NAME: DIRECT UV (280)

ID	ABS 280.0nm	CONC mg/ml
999	0.121	123.45
1	0.234	2345.6
2	0.345	345678

	PRINT LIST	SAVE DATA	TEST PAGE	CLEAR RESULTS

Warburg-Christian

The Warburg-Christian analysis is uses an absorbance difference measurement (at 280 and 260nm) to determine the concentration of protein in an unknown sample.

Test parameters

	WARBURG-CHRISTIAN			
TEST NAME				**WARBURG-CHRISTIAN**
WAVELENGTH 1				**280.0nm**
WAVELENGTH 2				**260.0nm**
PROTEIN FACTOR (λ1)				**1.550**
PROTEIN FACTOR (λ2)				**0.760**
DILUTION MULTIPLIER				**1.00**
UNITS				**mg/ml**
SAMPLE POSITIONER				**AUTO 6 + REF**
NUMBER OF SAMPLES				**1**
ID# (0-OFF)				**0**
LOW/HIGH LIMITS				**-9999/9999**
STATISTICS				**OFF**
AUTOPRINT				**OFF**
	PRINT TEST	**SAVE TEST**	**STORED TESTS**	**VIEW RESULTS**

Running Warburg-Christian measurements

- Place the blank in the correct cell position.
- With the Warburg-Christian parameter screen displayed, press **ZERO** to measure the blank.
- Place the unknown in the correct cell position.
- Press **RUN** to start the measurement. The Warburg-Christian measurement screen appears. When the instrument is finished measuring the absorbance of the sample, it displays the sample ID#, its absorbance at 280 and 260nm and its protein concentration on a screen like the one shown below.

TEST NAME: WARBURG-CHRISTIAN

ID	ABS(λ1) 280.0nm	ABS(λ1) 260.0nm			
999	0.123	0.456			
	PROTEIN CONC		=	1111.1	mg/ml
1	1.234	1.567			
	PROTEIN CONC		=	33.8	mg/ml

	PRINT LIST	SAVE DATA	TEST PAGE	CLEAR RESULTS

Cell growth measurements

The cell growth measurement uses absorbance at 600nm to indicate the progress of cell growth in a sample. The instrument does not perform any calculations or graphing for the data.

Test parameters

	CELL GROWTH			
TEST NAME				CELL GROWTH
WAVELENGTH				600.0nm
SAMPLE POSITIONER				AUTO 6 + REF
NUMBER OF SAMPLES				1
ID# (0-OFF)				0
LOW/HIGH LIMITS				-9999/9999
STATISTICS				OFF
AUTOPRINT				OFF
	PRINT TEST	SAVE TEST	STORED TESTS	VIEW RESULTS

Running cell growth measurement

- With the cell growth parameter screen displayed, select the required Sample Positioner mode, number of samples (if appropriate), and initial sample number (ID#).
- Place the blank in the correct cell position.
- Press **ZERO/BASE** to measure the blank.
- Place the unknown(s) in the correct cell position(s).
- Press **RUN** to start the measurement.
  When the instrument is finished measuring the absorbance of the sample, it displays the sample number and absorbance on the screen.

Oligo calculator functions

The oligonucleotide calculator determines the following data for a base sequence that you enter:

- Number of bases
- Percent GC content
- Molecular weight
- Absorptivity (ε)
- Conversion factor to be used in Oligonucleotide measurements.
- T_m for oligos up to 20-mers, DNA-DNA hybrids, DNA-RNA hybrids & RNA-RNA hybrids

Appendix C lists the parameters and formulae used for each of these calculations.

Specifying a base sequence

You will need to enter a base sequence before you can run the oligonucleotide calculations.

- With the Base Sequence screen displayed, press the Right/Left Arrow keys to select the required base.
- Press **ENTER** to add the base to the sequence.
- Repeat these steps until you have specified the entire base sequence. The displayed number of bases, percent GC content, molecular weight, absorptivity (ε), and conversion factor will be updated as each new base is added to the sequence.

Using the oligonucleotide calculator

- With the Base Sequence screen displayed, press **Tm CALC** to view the Melting Point calculator.
- Use the Up/Down Arrow keys to select any parameter to be changed, and then press **ENTER** to start the edit process.
- Once all parameters have been set appropriately, the relevant set of melting point predictions will be displayed.

SCAN

- To select Scan highlight the SCAN option on the General Tests Page and press ENTER. The SCAN Methods page is displayed and from here the instrument and analysis parameters can be set up.

- Move the cursor to the required parameter using the Up/Down Arrow keys. Press ENTER to enable a parameter to be changed.

- Once the method has been set up press ZERO/BASE to perform a baseline scan with the current method (see page 7) and then press RUN. The spectrophotometer will perform the scan and display the result on the SCAN GRAPH page. From here the spectrum can be manipulated and saved to Library or Disk. See the DATA STORE section for explanation of file functions.

SCAN PARAMETERS Page

Note: The current spectrum will be lost if any of the method parameters (except for the User name) are changed.

* SCAN *	
SCAN TYPE	**INTELLISCAN**
TEST NAME	**TEST 1**
MODE	**ABS**
START	**400.0 nm**
STOP	**600.0 nm**
BANDWIDTH	**2.0 nm**
SPEED	**NORMAL**
DATA INTERVAL	**1.0 nm**
PEAK TABLE	**OFF**
GRAPH HIGH	**2.000**
GRAPH LOW	**0.000**
SMOOTHING	**NONE**
LAMP CHANGE	**325 nm**
USER	**Name**
UVCALC	**0**
SAMPLE POSITIONER	**AUTO 7**
NUMBER OF SAMPLES	**2**

SCAN TYPE : Select from STANDARD / INTELLISCAN.

- Standard mode enables the setting of a given scan speed and data interval. Intelliscan mode sets the data interval automatically and varies the scan speed according to the Absorbance of the spectrum.

TEST NAME : Enter a description using the TEXT ENTRY screen.

- The Test Name identifies the method and will be saved with the method and any spectra produced by the method.

MODE : Select from ABS / %T / I / 1D / 2D / 3D / 4D.

ABS	Selects Absorbance.
%T	Selects % transmittance.
I	Selects Intensity mode. This will measure the intensity of the signal in the sample beam.
1D	Selects first derivative. This records the first derivative of the Absorbance spectrum.
2D	Selects second derivative. This records the second derivative of the Absorbance spectrum.

3D	Selects third derivative. This records the third derivative of the Absorbance spectrum.
4D	Selects fourth derivative. This records the fourth derivative of the Absorbance spectrum.

The current spectrum will be lost if the Scan Mode is changed.

START **:** Select a wavelength between 190.0 nm and 1096.0 nm.

- Selects start wavelength.

If the start wavelength requires the Deuterium lamp then this will be switched on. The Start wavelength must be at least 4 nm less than Stop wavelength. The current spectrum will be lost if the Start wavelength is changed.

STOP **:** Select a wavelength between 194.0 nm and 1100.0 nm.

- Selects stop wavelength.

The Stop wavelength must be at least 4 nm greater than the Start wavelength.
The current spectrum will be lost if the Stop wavelength is changed.

BANDWIDTH **:** This is fixed at 2.0 nm.

SPEED **:** Selection depends on Scan Type selected.

- In Intelliscan mode select from COLOUR /ZIP / SURVEY / NORMAL / QUANT.

- In Standard mode select from 3800, 2400, 1200, 600, 240, 120, 30, 10 or 1 nm per min.

DATA INTERVAL **:** Sets the frequency of data points in the spectrum. Selection depends on Scan Type.

In Intelliscan mode the data interval is fixed according to the intelliscan type selected.

Intelliscan	**Interval between points**
COLOUR	10nm
ZIP	4 nm
SURVEY	2 nm
NORMAL	1 nm
QUANT	0.5 nm
HIGH RES	0.2 nm

In Standard mode the choice of data interval depends on the scan speed selected.

Speeds	**Data Intervals**
3800	10, 4
2400	10, 4, 2
1200	10, 4, 2, 1
600	10, 4, 2, 1, 0.5
240	10, 4, 2, 1, 0.5, 0.2
120	10, 4, 2, 1, 0.5, 0.2
30	10, 4, 2, 1, 0.5, 0.2
10	10, 4, 2, 1, 0.5, 0.2
1	10, 4, 2, 1, 0.5, 0.2

The current spectrum will be lost if the scan speed is changed.

PEAK TABLE **:** Select from OFF / PEAKS / VALLEYS / PKS & VALLEYS / ZERO CROSS / TRACK / RATIO / CORR. RATIO / PEAK HEIGHT.

Note: RATIO, CORR RATIO, and PEAK HEIGHT do not appear on this menu when UVCalc has been installed**.** UVCalc can perform these calculations, if required, in addition to a wide range of additional data manipulations. See UVCalc Manual.

This selects the type of peak picking done automatically as part of the method. Results are reported on the Peaks Page. Peaks information is stored with any saved spectrum.

OFF Sets Peak Table to Off. No peaks information is produced as part of the scan.

PEAKS Picks the highest peaks in a spectrum up to a maximum of 10 peaks.

VALLEYS Picks the lowest troughs in a spectrum up to a maximum of 10 troughs.

PKS & VALLEYS Picks the 5 highest peaks and the 5 lowest valleys.

ZERO CROSS Picks all the points where the spectrum crosses zero up to a maximum of 10 crossing points.

TRACK This function allows the Absorbance (or other mode) values to be reported at up to 10 user selected wavelengths. To enter the desired wavelengths select PEAK TABLE TRACK then press VIEW GRAPH.

You do not have to have a spectrum present on the graph to enter the selected wavelengths. Press MANIPULATE and select TRACK. For each wavelength move the cursor to the desired position press ENTER. Once all the wavelengths have been entered go back to the SCAN METHOD page and save the method.

RATIO This function allows the ratio of the measurements at the two wavelengths to be automatically calculated at the end of the scan (e.g. $Abs(\lambda_1)/Abs(\lambda_2)$). To enter the desired wavelengths select PEAK TABLE and press ENTER then select RATIO. A pop up box appears in which to enter the first wavelength. Enter the desired wavelength and press ENTER. Repeat for the second wavelength. Once all the method parameters have been set, save the method.

CORR RATIO This function allows the ratio of measurements at two wavelengths to be calculated relative to that at a third wavelength automatically at the end of a scan (e.g. $(Abs(\lambda_1)–Abs(\lambda_3)) / (Abs(\lambda_2)–Abs(\lambda_3))$) . To enter the desired wavelengths select PEAK TABLE and press ENTER then select CORR RATIO. A pop up box appears in which to enter the first wavelength. Enter the desired wavelength and press ENTER. Repeat for the second and correction wavelengths. Once all the method parameters have been set save the method.

PEAK HEIGHT This function allows the height of a peak to be calculated relative to local baseline rather than y = 0. To enter the desired wavelengths select PEAK TABLE and press ENTER then select PEAK HEIGHT. A pop-up box appears in which to enter the wavelengths required. λ_1 and λ_3 define the baseline, λ_2 defines the peak. Once all the parameters have been set, save the method.

GRAPH HIGH: Select from range (GRAPH LOW + 0.01) to 6.00.
Sets the upper graph limits on the SCAN GRAPH page.

GRAPH HIGH must be 0.01 greater than GRAPH LOW.

GRAPH LOW **:** Select from range -0.3 to (GRAPH HIGH- 0.01).

Sets the lower graph limits on the SCAN GRAPH page.
GRAPH LOW must be 0.01 less than GRAPH HIGH.

SMOOTHING **:** Select from NONE, LOW, MEDIUM or HIGH.

Applies modified/improved Savitsky-Golay smoothing to the spectrum.

LAMP CHANGE **:** Select from 315, 320, 325, 330, 335, 340, D2, W.

Selects the wavelength at which the source is changed between the Tungsten and Deuterium lamps.
Selecting D2, or W overrides any changeover and the selected lamp will be used regardless of the wavelength set.

USER **:** Switches to the TEXT ENTRY screen.

The operator name is automatically saved with the method and any spectra produced by the method.
Changing the operator name will not cause the current spectrum to be lost.
If User Log-on is in operation, the operator name cannot be changed.

UVCALC **:** Appears when the UVCalc software has been installed. Switches to the UVCALC screen.

SAMPLE POSITIONER: Appears when the 7 Cell Changer is fitted. Select from AUTO 7 / AUTO 6 + REF. / MANUAL 7

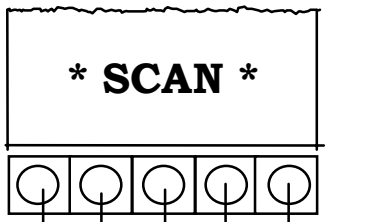
AUTO 7 — Up to 7 measurements may be made without changing the samples in the Cell Changer. After each sample measurement, the instrument automatically advances the Cell Changer to the appropriate position for the next sample.

AUTO 6 + REF — Up to 6 sample measurements may be made without changing the samples in the Cell Changer. The instrument automatically measures the blank (in position 1), then automatically advances the Cell Changer to the appropriate position for the next sample. Regardless of where the Cell Changer is positioned, when you press ZERO/BASE the Cell Changer automatically moves to position 1. After the blank measurement, it returns to its original position.

MANUAL 7 — Up to 7 measurements may be made without changing the samples in the Cell Changer, by using the left and right arrow keys to advance the Cell Changer to the next position.

NUMBER OF SAMPLES: Appears when the 7 Cell Changer is fitted, and an automatic operating mode has been selected. Valid range; 1-99.

SCAN PARAMETERS page function keys



VIEW RESULTS - Switches to the Scan Peak Table screen if any of the peak functions have been performed or the Track Table screen if track has been used.

VIEW GRAPH - Switches to the Scan Graph screen.

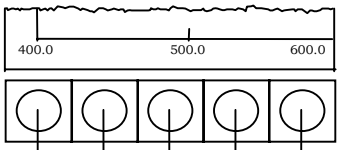
SAVE METHOD - Brings up the Filename Function screen and then saves the method including ID, operator name and track wavelengths if the PEAK TABLE parameter is set to TRACK.

PRINT METHOD - Prints the current method parameters on the printer

UVCALC RESULTS - Switches to UVCalc results screen if an equation has been entered and results are available. (Only available if UVCalc has been installed.)

SCAN GRAPH Page

- This page displays spectra and allows them to be manipulated.



VIEW RESULTS - Switches to the PEAK TABLE page.

SCAN PAGE - Returns to the SCAN page.

SAVE DATA - Displays the SAVE screen from where method and data can be saved to disk.

PRINT GRAPH - Provides a hardcopy of the results as shown on screen.

MANIPULATE - Displays the Manipulate options.

- Pressing RUN starts a scan using the current method.
- Pressing ZERO/BASE starts a baseline using the current method. (See page 7).

MANIPULATE OPTIONS

MANIPULATE
TRACK
RESCALE
COMPARE
MODE
PEAKS
SMOOTHING
ORIGINAL

TRACK Reports x and y axis values using the tracking cursor.

RESCALE Changes x and y axis scales automatically or manually.

COMPARE Loads reference spectrum for comparison.

MODE Changes mode. Select from %T / ABS / 1D / 2D / 3D / 4D.

PEAKS Finds spectral peaks. Select from PEAKS / VALLEYS / PEAKS & VALLEYS/ ZERO CROSS / RATIO / CORR. RATIO / PK HEIGHT.
(Ratio, Corr. Ratio and Pk. Height are not available when UVCalc has been installed.)

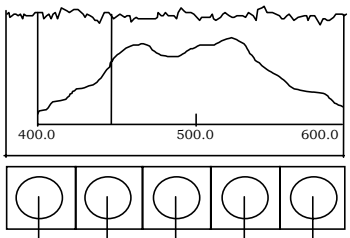
SMOOTHING Applies LOW, MEDIUM or HIGH modified/improved Savitsky-Golay smoothing to the spectrum.

ORIGINAL Resets the graph to display the data as originally collected.

TRACK

- To move the vertical cursor across the screen use the Left and Right Arrow keys. The cursor always moves to a data point regardless of the displayed scales. Pressing ENTER places a marker at the current wavelength. Up to 10 wavelengths can be selected.

TRACK page function keys



- Pressing CLEAR will delete markers in turn, highest number first.
- The x-axis values are listed on the TRACK table page. Further markers can be added to the spectrum at any time; however selecting TRACK will cause any previous PEAK TABLE information to be lost.

VIEW TABLE - Switches to the TRACK TABLE page.

FAST/SLOW - Toggles between two cursor speeds. In FAST mode the cursor jumps 5% of the graph or to the next data point whichever is the greater. In SLOW mode the cursor jumps to the next data point or the next display pixel whichever is the greater. The function key label shows the next speed ie the opposite to the one selected.

CLEAR ALL - Clears all the markers and the TRACK TABLE.

PRINT GRAPH - Provides a hardcopy of the results showing the markers and x and y-axis values.

SCAN GRAPH - Returns to the SCAN GRAPH page.

RESCALE

RESCALE
AUTO
GRAPH HIGH
GRAPH LOW
GRAPH START
GRAPH STOP
PROCEED

- This option gives pop-up menus for changing the graph x and y -axis scales.
- Move the cursor to one of the options and press ENTER to select an operation.

AUTO	Displays the SCAN GRAPH with the x and y-axes rescaled so that the Spectrum fills the screen.
GRAPH HIGH	Pops up a window for entry of the GRAPH HIGH limit.
GRAPH LOW	Pops up a window for entry of the GRAPH LOW limit.
GRAPH START	Pops up a window for entry of the required start wavelength.
GRAPH STOP	Pops up a window for entry of the required stop wavelength.
PROCEED	Used after GRAPH HIGH, GRAPH LOW, GRAPH START or GRAPH STOP to return to the SCAN GRAPH page with the graph rescaled using the new parameters.

COMPARE

- When selected, Compare goes to the LIBRARY page and displays a list of scan data files. Highlight the desired file using the Up/Down Arrow keys and press LOAD. The reference spectrum is displayed as a dotted trace.
- Once loaded the reference spectrum will remain on the screen (and will be printed) with all subsequent scans until removed. To remove the reference spectrum from the display, select MANIPULATE ORIGINAL or load a new method.

MODE: Select from ABS / %T / 1D / 2D / 3D / 4D.

ABS	Selects Absorbance.
%T	Selects % transmittance.
1D	Selects first derivative. This records the first derivative of the Absorbance spectrum.
2D	Selects second derivative. This records the second derivative of the Absorbance spectrum.
3D	Selects third derivative. This records the third derivative of the Absorbance spectrum.
4D	Selects fourth derivative. This records the fourth derivative of the Absorbance spectrum.

PEAKS

FUNCTION
PEAKS
VALLEYS
PKS & VALLEYS
ZERO CROSS
RATIO
CORR RATIO
PK. HEIGHT

- This option enables the spectrum to be automatically searched for peaks, valleys or zero crossing points. Move the cursor to one of the options and press ENTER to perform a search. When the search is complete the spectrum is displayed with the peak positions marked. For a peak to be found there must be more than 15 data points between that point and a previous peak.

For RATIO and CORR RATIO enter the wavelengths as prompted. All results can be viewed by pressing ○○○○● VIEW RESULTS.

PEAKS	Marks the 10 highest peaks.
VALLEYS	Marks the 10 lowest valleys.
PKS&VALLEYS	Marks the 5 highest peaks and 5 lowest valleys.
ZERO CROSS	Marks the first 10 zero crossings.
RATIO	Calculates the ratio λ_1/λ_2.
CORR RATIO	Calculates the ratio $(\lambda_1-\lambda_3)/(\lambda_2-\lambda_3)$.
PK HEIGHT	Calculates the peak maximum relative to a local baseline.

(Ratio, Corr. Ratio and Pk. Height are not available when UVCalc has been installed.)

SMOOTHING

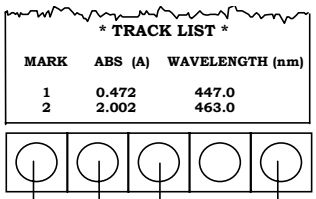
- This option offers a pop-up menu to choose one of three smoothing algorithms. Choices are NONE, LOW, MEDIUM and HIGH. A Savitsky-Golay smooth is performed on the data and in each case data points will be lost from either end of the data.

SMOOTHING	No of POINTS USED	POINTS LOST AT EACH END
NONE	0	0
LOW	9	4
MEDIUM	17	8
HIGH	33	16

ORIGINAL

- This removes any manipulation and displays the spectrum as originally collected and specified by the scan method. It will also clear any Compare spectrum.

TRACK TABLE Page



- The list shows the y-axis values of the spectrum for the wavelengths marked during TRACK. The measured values will be ABS, %T, INTENSITY or 1D / 2D / 3D / 4D depending on the current mode.

VIEW GRAPH - Switches to the TRACK page.

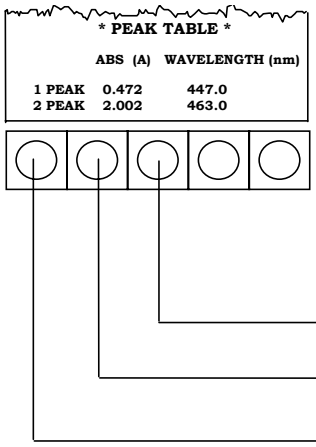
LIMS EXPORT – Sends the results via the RS232 port.

PRINT LIST - Prints the list on the selected printer.

SCAN GRAPH - Returns to the SCAN GRAPH page.

- If a spectrum is saved then the track markers are also saved and will be displayed when the spectrum is reloaded.

PEAK TABLE Page



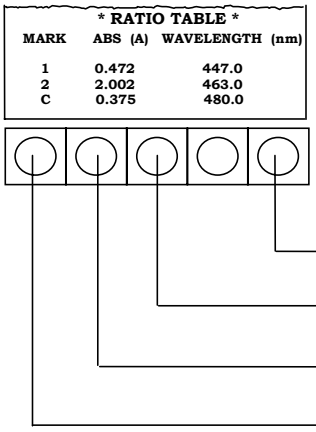
- The list shows the positions and values of the peaks as calculated by the function selected in MANIPULATE PEAKS. The measured values will be ABS, %T, INTENSITY or 1D / 2D / 3D / 4D depending on the current mode and are sorted by wavelength. Each marker is identified as a peak, valley or zero crossing.

LIMS EXPORT – Sends the results via the RS232 port.

PRINT LIST - Prints the list on the selected printer.

SCAN GRAPH - Returns to the SCAN GRAPH page.

RATIO TABLE Page



- The page shows the positions and values of the wavelengths and the ratio as selected by the RATIO or CORR RATIO functions. (Not available if UVCalc has been installed.)

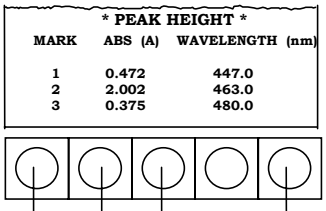
VIEW GRAPH - Returns to the SCAN GRAPH page.

LIMS EXPORT – Sends the results via the RS232 port

PRINT LIST - Prints the list on the selected printer.

SCAN GRAPH - Returns to the SCAN GRAPH page.

PEAK HEIGHT Page



- This page shows the position and values of the wavelengths and the peak height as selected by the PEAK HEIGHT function. (Not available if UVCalc has been installed.)

VIEW GRAPH - Returns to the SCAN GRAPH page.

LIMS EXPORT – Sends results via the RS232 port.

PRINT LIST - Prints the list on the selected printer.

SCAN GRAPH - Returns to the SCAN GRAPH page.

FIXED

- Instrument and analysis parameters are set up on the FIXED page. Move the cursor to the required parameter using the Up/Down Arrow keys. Change the parameter by pressing the ENTER key.

- Once the method has been set up, ensure that both sample and reference beams are clear or contain blank samples. Press ZERO/BASE to zero the instrument for the current method, then insert the sample and press RUN. The spectrophotometer will perform a measurement and display the result on the FIXED RESULTS page.

- Once all results have been collected, save the data.

FIXED METHOD Page

* FIXED *	
MODE	**ABS**
TEST NAME	
λ SELECT	**SINGLE λ**
WAVELENGTH(S)	**550.0 nm**
BANDWIDTH	**2.0 nm**
INTEGRATION	**1 s**
DELAY TIME	**00:00**
LAMP CHANGE	**325 nm**
USER	
UVCALC	**0**
SAMPLE POSITIONER	**AUTO 7**
NUMBER OF SAMPLES	**2**

MODE : Select from ABS / %T / CONC.

ABS	Selects Absorbance.
%T	Selects % transmittance.
CONC	Selects Concentration mode. (Only available when SINGLE λ is selected and not available if UVCalc is installed)

- CONC allows the result to be automatically multiplied by a factor to give concentration measurements. If selected two further parameters are added to the method, FACTOR and UNITS.

TEST NAME : Enter a description using the TEXT ENTRY screen.

- The Test Name identifies the method and will be saved with the method and any results produced by the method.

λ SELECT : Select from SINGLE λ /MULTI λ /SERIAL λ.

SINGLE λ	This option is used to measure each sample at a single wavelength which is the same for each sample.
MULTI λ	This option allows each sample to be measured at up to 20 wavelengths, which are the same for each sample.
SERIAL λ	This option allows a single wavelength measurement to be made at a different wavelength on up to 9 samples.

WAVELENGTH(S) :

SINGLE λ Use the numeric key pad to enter the required wavelength into the pop-up box. Press ENTER when finished.

MULTI λ Use the up and down arrow keys to move to the wavelength to be entered or edited and press ENTER to display the edit box. Use the numeric keypad to enter the wavelength and press ENTER when finished. The instrument returns to the MULTI λ screen with the next wavelength in the list highlighted. Up to 20 wavelengths may be entered. When the list is finished press the ACCEPT function key to accept the new list or the CANCEL function key to return to the FIXED METHOD page without changing the wavelength list.

SERIAL λ Press ENTER to display the edit box for the wavelength to be used for the first sample. Data entry is as for MULTI λ above. When the required wavelengths have been entered press ACCEPT to accept the new list, or press CANCEL to return to the FIXED METHOD page leaving the original list unchanged.

If the wavelength requires the Deuterium lamp then this will be switched on. The current data will be lost if the wavelength is changed.

BANDWIDTH : This is fixed at 2.0 nm.

INTEGRATION : Enter integration time in seconds.

- This sets the integration time for which the result is measured.

The current data will be lost if the integration time is changed.

DELAY TIME : Set a time in the range 00.05 to 99.59, using . to separate minutes and seconds.

- This sets the time between pressing RUN and the start of the measurement. The range is from 0 to 99 minutes and 59 seconds.

LAMP CHANGE : Select from 315, 320, 325, 330, 335, 340, D2, W.

Selects the wavelength at which the source is changed between the Tungsten and Deuterium lamps. Selecting D2, or W overrides any changeover and the selected lamp will be used regardless of the wavelength set.

FACTOR : Enter the factor for the concentration.

Only available in CONC mode, the factor is used to multiply the absorbance result to produce a concentration result. Changing the factor will not cause current results to be lost. They will be recalculated using the new factor.
CONC mode is not available when UVCalc has been installed or when MULTI λ or SERIAL λ is selected.

UNITS : Enter units for concentration using the TEXT ENTRY page.

Only available in CONC mode; used to enter the required description of the concentrations up to 11 alphanumeric characters.

USER **:** Switches to the TEXT ENTRY screen.

- The operator name is automatically saved with the method and any data produced by the method.

Changing the User name will not cause any current data to be lost.
N.B. If user log-on is in operation, the User name cannot be changed.

UVCALC **:** Switches to the UVCALC screen (if installed).

SAMPLE POSITIONER: Appears when the 7 Cell Changer is fitted. Select from AUTO 7 / AUTO 6 + REF. / MANUAL 7

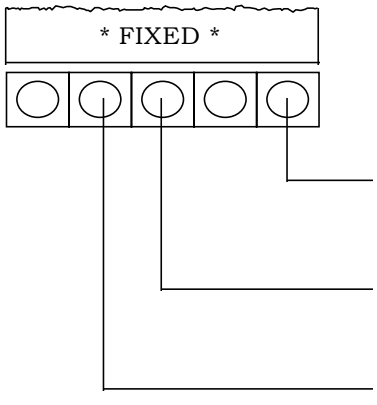
AUTO 7 — Up to 7 measurements may be made without changing the samples in the Cell Changer. After each sample measurement, the instrument automatically advances the Cell Changer to the appropriate position for the next sample.

AUTO 6 + REF — Up to 6 sample measurements may be made without changing the samples in the Cell Changer. The instrument automatically measures the blank (in position 1), then automatically advances the Cell Changer to the appropriate position for the next sample. Regardless of where the Cell Changer is positioned, when you press ZERO/BASE the Cell Changer automatically moves to position 1. After the blank measurement, it returns to its original position.

MANUAL 7 — Up to 7 measurements may be made without changing the samples in the Cell Changer, by using the left and right arrow keys to advance the Cell Changer to the next position.

NUMBER OF SAMPLES: Appears when the 7 Cell Changer is fitted, and an automatic operating mode has been selected. Valid range; 1-999.

FIXED Method Page Function Keys



VIEW RESULTS - Switches to the FIXED RESULTS page.

SAVE METHOD - Brings up the SAVE page from where the method can be saved to Disk.

PRINT METHOD - Prints the current method parameters on the printer.

- Pressing RUN starts a fixed measurement using the current method and switches to the FIXED RESULTS page.

- Pressing ZERO starts a zero using the current method. (See page 7).

Any changes to the WAVELENGTH, BANDWIDTH, INTEGRATION or LAMP CHANGE parameters will invalidate the current results.

If AUTOPRINTING is selected (see SETUP for details), a change to the MODE parameter will invalidate the current results.

FIXED RESULTS Page

- The layout of the page depends on the Mode and λ Select in use.

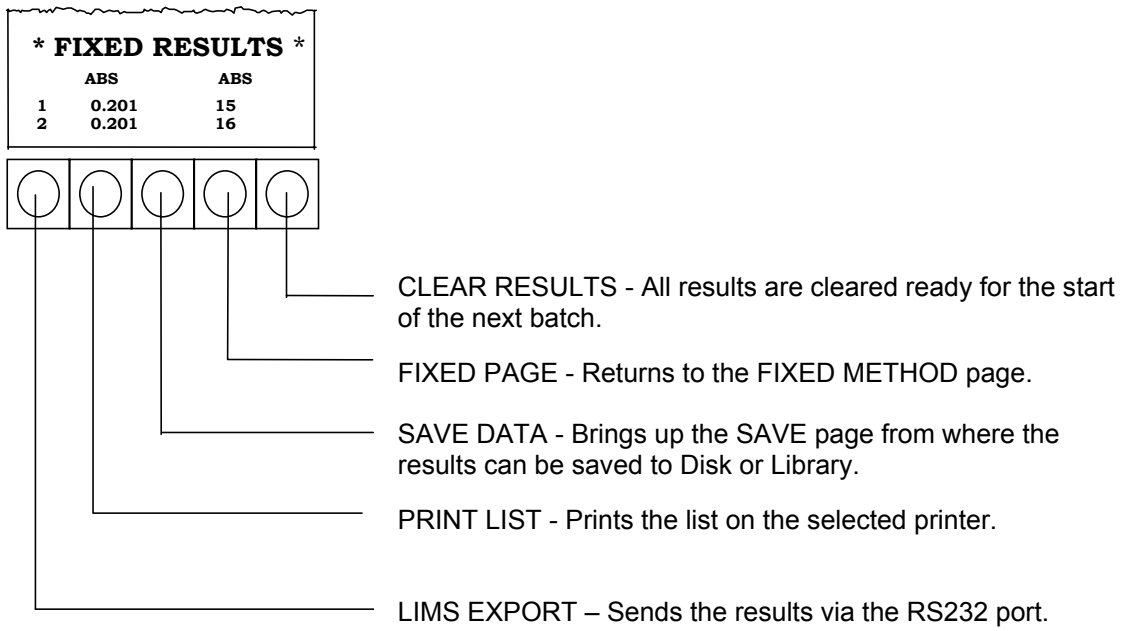
  SINGLE λ In ABS or %T modes up to 2 columns of results are displayed per page.In CONC mode a single column of results is displayed on each page. Results accumulate on the same page until it is full.

  MULTI λ Two columns of results are displayed per page. Results of each sample always start on a new page.

  SERIAL λ One column of results is displayed per page. Results accumulate on the same page until it is full.

- To move up or down pages of results use the Up/Down arrow keys.

- Results are numbered sequentially from 1 to 600. Conc values are from 0.0001 to 9999.9. Any concentration value outside this range is marked "UNDER RANGE" or "OVER RANGE".


* FIXED RESULTS *
ABS ABS
1 0.201 15
2 0.201 16
CLEAR RESULTS - All results are cleared ready for the start of the next batch.
FIXED PAGE - Returns to the FIXED METHOD page.
SAVE DATA - Brings up the SAVE page from where the results can be saved to Disk or Library.
PRINT LIST - Prints the list on the selected printer.
LIMS EXPORT – Sends the results via the RS232 port.

- Press RUN to take another sample measurement.

- Press ZERO/BASE to zero the instrument at the wavelength(s) specified in the method. (See page 7).

QUANTIFICATION

Instrument and analysis parameters are set up on the QUANT page. Move the cursor to the required parameter using the Up/Down Arrow keys. Change the parameter by pressing the ENTER key.

- Once all results have been collected, save the data.

QUANT METHOD Page

* QUANT *	
TEST NAME	
WAVELENGTH	**550.0 nm**
BANDWIDTH	**2.0 nm**
INTEGRATION	**1 s**
STANDARDS	**3**
REPLICATES	**1**
UNITS	
CURVE FIT	**LINEAR**
LAMP CHANGE	**325 nm**
USER	
UVCALC	**0**
MEASURE STDS	**YES**
SAMPLE POSITIONER	**AUTO 7**
NUMBER OF SAMPLES	**2**

TEST NAME : Enter a description using the TEXT ENTRY screen.

- The Test Name identifies the method and will be saved with the method and any results produced by the method.

WAVELENGTH : Select a wavelength between 190.0 nm and 1100.0 nm.

If the wavelength requires the Deuterium lamp then this will be switched on. The current data will be lost if the wavelength is changed.

BANDWIDTH : This is fixed at 2.0 nm.

INTEGRATION : Enter integration time in seconds.

This sets the integration time for which the result is measured.
The current data will be lost if the integration time is changed.

STANDARDS : Brings up the Standards Entry Page

Use the up and down arrow keys to move through the list of standards. When the standard to be entered or edited is highlighted, press ENTER to display the Edit pop-up. Use the numeric keys to enter the concentration of the standard and press ENTER when finished. The instrument returns to the Standards Entry page with the highlight on the next standard on the list. Up to 20 standards can be specified.

Changing the standards will cause any current data to be lost.

REPLICATES : Enter number of replicates for each standard.

- Sets the number of times each standard is measured (maximum 3). Each value obtained is used in the calibration.

UNITS : Enter units for concentration using the TEXT ENTRY page.

CURVE FIT **:** Select from LINEAR / LINEAR TO 0 / QUADRATIC / QUAD TO 0.

- Selects the curve fit algorithm used in the calibration.

LINEAR	performs a linear calibration. At least two standards are required.
LINEAR TO 0	performs a linear calibration forced through zero.
QUADRATIC	performs a quadratic fit on the data. At least three standards are required.
QUAD TO 0	performs a quadratic fit with the data forced through zero. At least two standards are required.

Changing the curve fit will cause the existing calibration to be recalculated.
Any results associated with the previous calibration will be lost.

LAMP CHANGE **:** Select from 315, 320, 325, 330, 335, 340, D2, W.

- Selects the wavelength at which the source is changed between the Tungsten and Deuterium lamps. Selecting D2, or W overrides any changeover and the selected lamp will be used regardless of the wavelength set.

Any current data will be lost if the lamp changeover wavelength is changed

USER **:** Switches to the TEXT ENTRY screen.

The User name is automatically saved with the method and any data produced by the method.
Changing the User name will not cause any current data to be lost.
If User Log-on is in operation, the User name cannot be changed.

UVCALC **:** Switches to the UVCALC screen.

- Only available if UVCalc is installed. See UVCalc Manual.

MEASURE STDS **:** Toggles between YES and NO.

- When YES, and Standard concentrations have been entered from the Quant Standards page, pressing Calibrate causes the instrument to prompt the user to put the standard in the beam and press Run to measure, for each Standard in turn.

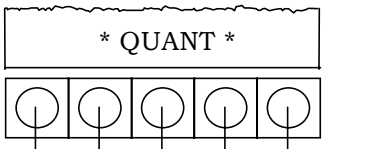
- When NO, pressing Calibrate causes the system to prompt for an absorbance to be entered manually for each Standard, effectively enabling a calibration originating elsewhere to be entered.

SAMPLE POSITIONER: Appears when the 7 Cell Changer is fitted. Select from AUTO 7 / AUTO 6 + REF. / MANUAL 7

AUTO 7	Up to 7 measurements may be made without changing the samples in the Cell Changer. After each sample measurement, the instrument automatically advances the Cell Changer to the appropriate position for the next sample.
AUTO 6 + REF	Up to 6 sample measurements may be made without changing the samples in the Cell Changer. The instrument automatically measures the blank (in position 1), then automatically advances the Cell Changer to the appropriate position for the next sample. Regardless of where the Cell Changer is positioned, when you press ZERO/BASE the Cell Changer automatically moves to position 1. After the blank measurement, it returns to its original position.

MANUAL 7	Up to 7 measurements may be made without changing the samples in the Cell Changer, by using the left and right arrow keys to advance the Cell Changer to the next position.
NUMBER OF SAMPLES:	Appears when the 7 Cell Changer is fitted, and an automatic operating mode has been selected. Valid range; 1-999.

QUANT Page function keys



VIEW CALIB - Switches to the QUANT GRAPH page if a valid calibration exists.

VIEW RESULTS - Switches to the Quant Results page if there are any sample results.

SAVE METHOD - Brings up the SAVE page from where the method can be saved to Disk.

PRINT METHOD - Prints the current method parameters and the standards table on the printer.

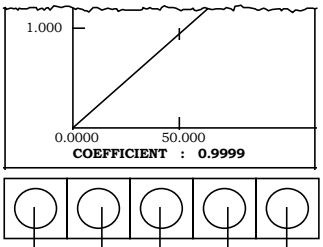
CALIBRATE – Starts the calibration process.

STANDARDS ENTRY Page

- Select STANDARDS on the Quant Method page to display the Standards Entry Page.
- This page lists the standards as defined in the QUANT METHOD. Before the system can be calibrated each standard must have a concentration entered.
- To enter Standard concentrations use the up and down arrow keys to move through the list of standards. When the standard to be entered or edited is highlighted press ENTER to display the Edit pop-up. Use the numeric keys to enter the concentration of the standard and press ENTER when finished. The instrument returns to the Standards Entry Page with the highlight on the next standard on the list. Up to 20 standards can be specified. When all the standards have been entered, press the ACCEPT function key to return to the QUANT Page with the new list of standards, or CANCEL to return leaving the old list unchanged.

QUANT CALIBRATION

- Press ZERO/BASE to zero the instrument with the current method. (See page 7).
- To calibrate the system press return to the QUANT page and press CALIBRATE. The QUANT CALIBRATION graph will be displayed and the instrument will prompt for each standard (and replicate) in turn. As the measurements of the standards proceed the datapoints are marked on the graph. When all the standards have been measured the system calculates the equation, rescales the graph then draws and displays the line of best fit on the graph.
- A calibration can be stopped by pressing the STOP function key. The calibration will be aborted and the software will return to the QUANT STANDARDS page. Any values obtained will be lost.
- If a calibration has not been done pressing RUN causes the warning prompt "CANNOT RUN WITHOUT CALIBRATION" to appear, otherwise it takes a sample measurement and switches to the Quant Results screen.



VIEW RESULTS - Switches to the Quant Results page if there are results.

QUANT PAGE - Switches back to the Quant page.

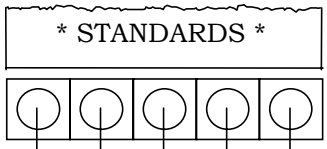
STANDARDS - Switches to the Quant Standards page.

PRINT GRAPH - Prints the Quant method and calibration graph.

SAVE METHOD - Switches to the SAVE page.

QUANT STANDARDS Page

- Press STANDARDS on the Quant Calibration Graph Page to display the Quant Standards Page.
- This page displays the measurements for each standard, and the equation of line and correlation coefficient for the curve fit.



VIEW CALIB - Switches to the QUANT GRAPH page if a valid calibration exists

VIEW RESULTS - Switches to the QUANT RESULTS page if there are any results in the table.

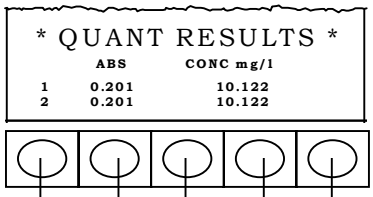
QUANT PAGE - Switches back to the Quant page.

EDIT STD – Available after calibration. Allows each standard to be used, ignored or remeasured.

EDIT CURVE – Available after calibration. Allows curve fit to be changed.

QUANT RESULTS Page

- To view further pages of results use the Up and Down arrow keys.
- Pressing RUN takes another sample measurement and displays the result.
- Results are numbered sequentially and any batch can be of up to 600 samples.



CLEAR RESULTS - Deletes all results from the results table.

QUANT PAGE - Switches back to the Quant page.

SAVE DATA - Brings up the SAVE page.

PRINT RESULTS - Gives a printout of the results.

LIMS EXPORT– Sends the results via the RS232 port.

RATE

- To select Rate highlight the RATE option on the GENERAL TESTS page and press ENTER. The RATE Methods page is displayed and from here the instrument and analysis parameters can be set up.

- Move the cursor to the required parameter using the Up/Down Arrow keys. Press ENTER to enable a parameter to be changed.

- Once the method has been set up press RUN. The spectrophotometer will perform the rate and display the result on the RATE GRAPH page. From here the data can be manipulated and saved to Disk.

RATE PARAMETERS Page

Note: The current data will be lost if any of the method parameters (except for the ID, Slope, Factor, Units and User name) are changed.

* RATE *	
TEST NAME	**TEST 1**
RATE MODE	**PARALLEL**
WAVELENGTH	**340.0 nm**
BANDWIDTH	**2.0 nm**
MEASURE INTERVAL	**00:30**
DELAY TIME	**00:00**
SLOPE	**POSITIVE**
RANGE	**0.5**
FACTOR	**1.000**
UNITS	**I/U**
LAMP CHANGE	**325 nm**
USER	**Name**
NUMBER OF SAMPLES	**7**
MEASURE CYCLES	**10**

TEST NAME : Enter a description using the TEXT ENTRY screen.

- The Test Name identifies the method and will be saved with the method and any results produced by the method.

RATE MODE : Toggles between SERIAL /PARALLEL when 7 Cell Changer is installed. Fixed at SERIAL for single cell holders.

SERIAL — Each sample is measured individually. In this mode, MEASURE TIME replaces MEASURE INTERVAL and sets the total time over which the sample is measured.

PARALLEL — Rate measurements for up to 7 samples may be made in parallel. In this mode, MEASURE INTERVAL sets the time between each cycle, i.e. the length of time between successive measurements on the first sample. The number of measurements taken on each sample is set by the MEASURE CYCLES parameter. The total time over which the measurements are made is the product of the MEASURE INTERVAL and the MEASURE CYCLES. For example an analysis using 4 cells with MEASURE INTERVAL set to 15 seconds and MEASURE CYCLES set to 20 would give a total measurement time of 5 minutes.

WAVELENGTH : Select a wavelength between 190 nm and 1100 nm.

- If a wavelength is selected that requires the Deuterium lamp then this will automatically be switched on. Any current data will be lost if the wavelength is changed.

BANDWIDTH : This is fixed at 2.0 nm.

MEASURE TIME : Set a time in the range 00:05 to 99:59.

- For SERIAL Rate measurements, this sets the time over which the sample will be measured. The range is from 5 seconds to 99 minutes and 59 seconds in steps of 1 second.

MEASURE INTERVAL: Set a time in the range 00:05 to 99:59.

- For PARALLEL Rate measurements, the measurement time sets the time between individual measurements on the first cell (i.e. the time for each measurement cycle).

DELAY TIME : Set a time in the range 00:05 to 99:59.

This sets the time between pressing RUN and the start of the measurement. The range is from 0 to 99 minutes and 59 seconds in steps of 1 second.

SLOPE : Select from POSITIVE or NEGATIVE.

- Sets the graph to display positive or negative changes in Absorbance. Choose POSITIVE if Absorbance increases with time. Choose NEGATIVE if Absorbance decreases with time.

RANGE : Set a number in the range 0 to 3A.

- This sets the graph y-axis. Enter a number slightly larger than the change in Absorbance expected.

FACTOR : Enter the factor for Activity as a number in the range 0.001 to 9999.999.

UNITS : Enters the units of Activity using the TEXT ENTRY page.

- Enters the required description or units of Activity up to 11 alphanumeric characters.

LAMP CHANGE : Select from 315, 320, 325, 330, 335, 340, D2, W.

- Selects the wavelength at which the source is changed between the Tungsten and Deuterium lamps. Selecting D2, or W overrides any changeover and the selected lamp will be used regardless of the wavelength set.

USER : Switches to the TEXT ENTRY screen.

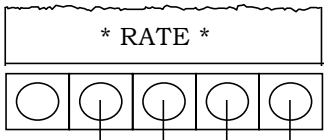
- The User name is automatically saved with the method and any data produced by the method.

Changing the User name will not cause the current data to be lost.
If User Log-on is in operation, the User name cannot be changed.

NUMBER OF SAMPLES: For PARALLEL Rate measurements: Valid range; 2-7.

MEASURE CYCLES : For PARALLEL Rate measurements: Valid range; 1-300.

RATE PARAMETERS Page function keys



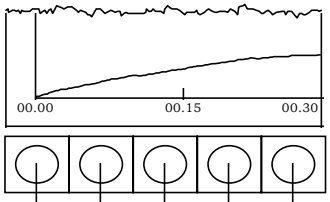
VIEW RESULTS - Goes to the RATE RESULTS page.

VIEW GRAPH - Goes to the RATE GRAPH page.

SAVE METHOD - Brings up the SAVE page from where the method can be saved to disk.

PRINT METHOD - Prints the current method parameters on the printer.

RATE GRAPH Page



- This page displays the RATE curve and allows it to be manipulated.

VIEW RESULTS - Switches to the RATE RESULTS page.

RATE PAGE - Returns to the RATE PARAMETERS page.

SAVE DATA - Brings up the SAVE screen from where method and data can be saved to disk.

PRINT - Provides a hardcopy of the results i.e. RATE GRAPH and RATE RESULTS.

MANIPULATE - Brings up the Manipulate options.

- Parallel Rate results have three printing options: ALL OVERLAY, ALL SEQUENTIAL, and ONE RESULT.

ALL OVERLAY Prints the results of all cells in the run together in batches of 4 (3 if using the internal printer). TRACK and SECTION markers are not included.

ALL SEQUENTIAL Prints each result in the run separately. TRACK and SECTION markers are included.

ONE RESULT Prints the result currently displayed. TRACK and SECTION markers are included.

- Pressing RUN starts a measurement using the current method.

- Pressing ZERO/BASE zeros the instrument using the wavelength specified in the current method. (See page 7).

MANIPULATE

MANIPULATE
TRACK SECTION RESCALE SMOOTHING ABS DISPLAY ORIGINAL ANOTHER CELL

TRACK Sets the start and stop time for the rate calculations.

SECTION Sets sequential start and stop times to enable rates to be calculated on up to four sections of the rate curve.

RESCALE Changes y-axis scale automatically or manually.

SMOOTHING Allows three levels of smoothing to be applied to the Rate Curve.

ABS DISPLAY Sets the display of absolute absorbance values or absorbances relative to the first measurement(s) of the run.

ORIGINAL Resets the graph to display the data as originally collected.

ANOTHER CELL Parallel Rate measurements only: Enables the results of another sample from the same run to be displayed.

TRACK

- To move the vertical cursor across the screen use the Left and Right Arrow keys. The cursor always moves to a data point regardless of the displayed scales. Pressing ENTER places a marker at the current time.

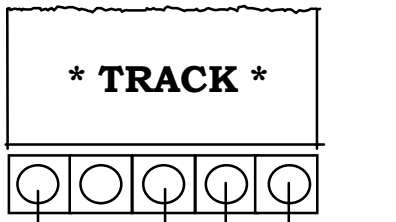
- To delete a marker, place the cursor on the marker and press CLEAR.

- The x-axis values are used to recalculate the rate of change of Absorbance between the new start and stop times. Results are listed on the RATE RESULTS page.

Up to four discrete pairs of cursors can be placed on the graph. Arrows are placed on the cursors and results are displayed on the RATE RESULTS page for those parts of the graph indicated by the arrows.

- Selecting SECTION will remove the TRACK markers.

- The minimum interval between TRACK cursors is one second.



VIEW RESULTS - Switches to the RATE RESULTS page.

FAST/SLOW - Toggles between two cursor speeds. In FAST mode the cursor jumps 5% of the graph or to the next data point whichever is the greater. In SLOW mode the cursor jumps to the next data point or the next display pixel whichever is the greater.The function key label shows the next speed ie the opposite to the one selected.

CLEAR ALL - Clears all the markers.

RATE GRAPH - Returns to the RATE GRAPH page.

SECTION

- To move the vertical cursor across the screen use the Left and Right Arrow keys. The cursor always moves to a data point regardless of the displayed scales. Pressing ENTER places a marker at the current time.

- To delete a marker place the cursor on the marker and press CLEAR.

Up to five markers can be placed on the graph. Rate results will be reported between markers providing a maximum of four sets of results (Sections). The minimum Section size is one second.
Results are listed on the RATE RESULTS page.

Selecting TRACK will remove the SECTION markers.

RESCALE

- This option gives a pop-up menu for changing the graph y -axis scale.

- Move the cursor to one of the options and press ENTER to select an operation.

The rescale options depend on whether Absolute or Relative Absorbance has been selected.

Absolute Absorbance:

RESCALE
AUTO GRAPH HIGH GRAPH LOW

AUTO - Displays the RATE GRAPH with the y-axis rescaled so that the trace fills the screen.

GRAPH HIGH, GRAPH LOW – Allow the user to set the upper and lower limits for the RATE GRAPH y-axis.

Relative Absorbance:

RESCALE
AUTO RANGE

AUTO - Displays the RATE GRAPH with the y-axis rescaled so that the trace fills the screen.

RANGE - Allows the user to set the upper y-axis value.

ABS DISPLAY

- This option enables the RATE GRAPH to be redisplayed with Absolute Absorbance or Relative Absorbance values.

SMOOTHING

- This option offers a pop-up menu to choose one of three smoothing algorithms. Choices are NONE, LOW, MEDIUM and HIGH. A moving point average is performed on the data and in each case data points will be lost from either end of the data.

SMOOTHING	No of POINTS USED	POINTS LOST AT EACH END
NONE	0	0
LOW	9	4
MEDIUM	17	8
HIGH	37	18

ORIGINAL

This removes any manipulation and displays the rate graph as originally specified by the rate method.

ANOTHER CELL

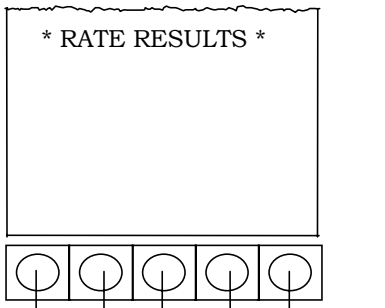
- If more than one rate has been run in parallel using the 7 Cell Changer then this function allows the results from any cell in the run to be selected and displayed. Enter the number of cell for which you wish to display results.

RATE RESULTS Page

- The Rate Results page displays the Initial and Final Absorbance, Initial and Final Time, the change in absorbance per minute, calculated Activity, Correlation Coefficient of the best fit line and finally the smoothing parameter used.

If the rate curve has been tracked the Initial and Final Absorbance with the Initial and Final Time will reflect those chosen by the two cursors.

Shown below is the Rate Results page after choosing 'SECTION' and the three sets of data represent results calculated for each section. A similar display will be seen with TRACK**.**



VIEW GRAPH - Returns to the RATE GRAPH page.

RATE PAGE - Returns to the RATE PARAMETERS page.

SAVE DATA - Brings up the SAVE screen from where method and data can be saved to disk.

PRINT - Provides a hardcopy of the results i.e. RATE GRAPH and RATE RESULTS.

LIMS EXPORT – Sends the results via the RS232 port.

- For Parallel Rate measurements, to view the result of any other sample press MANIPULATE on the RATE GRAPH page and select ANOTHER CELL.
- To print the results press PRINT on either the RATE GRAPH page or the RATE RESULTS page.

MCA

- The MCA (Multi Component Analysis) application is able to measure up to 20 components in a mixture, measuring up to 20 wavelengths per sample.

- Standards can be measured at run time or loaded from files obtained using the MULTI λ function of the FIXED application.

MCA METHOD Page

* MCA *	
TEST NAME	**TEST 1**
MEASURE STDS	**YES**
STANDARDS	**0**
UNITS	
WAVELENGTH(S)	**1**
BANDWIDTH	**2.0nm**
INTEGRATION	**1s**
DELAY TIME	**00**
LAMP CHANGE	**325nm**
USER	**Name**
SAMPLE POSITIONER	**AUTO 7**
NUMBER OF SAMPLES	**2**

TEST NAME : Enter a description using the TEXT ENTRY screen.

MEASURE STDS : Use ENTER to toggle between YES and NO.

YES - Standards are measured with the run and all fields remain editable.

NO - Standards are loaded from Library or Disk. The Wavelength(s), Bandwidth, Integration, Delay time, Lamp change and Operator Name are also loaded with the standards and cannot be edited. Any attempt to do so causes the prompt “Change method by loading MCA standards” to appear and no action is taken.

Changing the MEASURE STANDARDS parameter will cause all previous data to be lost.

STANDARDS : Switches to the STANDARDS ENTRY screen.

- Identifications and concentrations of up to 20 standards may be entered.

UNITS : Switches to the TEXT ENTRY screen.

- Enter the units for the concentration.

WAVELENGTH(S) : Select a wavelength between 190nm and 1100nm

If the wavelength requires the Deuterium lamp then this will be switched on. The current data will be lost if the wavelength is changed.

BANDWIDTH : This is fixed at 2.0nm.

INTEGRATION : Enter integration time in seconds.

- This sets the integration time for which the result is measured. The minimum is 1s, and the maximum is 9999s.

The current data will be lost if the integration time is changed.

DELAY TIME : Set a time in the range 00.00 to 99.59, using . to separate minutes and seconds. The number of seconds must always be entered explicitly.

- This sets the time between pressing RUN and the start of the measurement. The range is from 0 to 99 minutes and 59 seconds.This field is only available if UVCalc has been installed.

LAMP CHANGE : Select from 315, 320, 325, 330, 335, 340, D2, W.

- Selects the wavelength at which the source is changed between the Tungsten and Deuterium lamps. Selecting D2 or W overrides any changeover and the selected lamp will be used regardless of the wavelength set.

The current data will be lost if the lamp change parameters are changed.

USER : Switches to the TEXT ENTRY screen.

- The User name is automatically saved with the method and any data produced by the method.

Changing the User name will not cause any current data to be lost.
If User Log-on is in operation, the User name cannot be changed.

SAMPLE POSITIONER: Appears when the 7 Cell Changer is fitted. Select from AUTO 7 / AUTO 6 + REF. / MANUAL 7

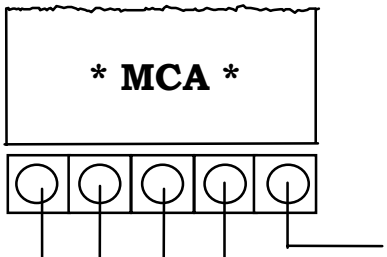
AUTO 7 Up to 7 measurements may be made without changing the samples in the Cell Changer. After each sample measurement, the instrument automatically advances the Cell Changer to the appropriate position for the next sample.

AUTO 6 + REF Up to 6 sample measurements may be made without changing the samples in the Cell Changer. The instrument automatically measures the blank (in position 1), then automatically advances the Cell Changer to the appropriate position for the next sample. Regardless of where the Cell Changer is positioned, when you press ZERO/BASE the Cell Changer automatically moves to position 1. After the blank measurement, it returns to its original position.

MANUAL 7 Up to 7 measurements may be made without changing the samples in the Cell Changer, by using the left and right arrow keys to advance the Cell Changer to the next position.

NUMBER OF SAMPLES: Appears when the 7 Cell Changer is fitted, and an automatic operating mode has been selected. Valid range; 1-999.

MCA PARAMETERS Page function keys



VIEW RESULTS - Transfers to the Results Table if it contains results.

VIEW STDS - Transfers to Standards results table if a calibration has been performed.

SAVE METHOD - Brings up the SAVE page from where the method can be saved to Disk.

PRINT METHOD - Prints the current method parameters on the printer.

CALIBRATE - Moves to the CALIBRATION PAGE to perform a calibration if standards and wavelengths have been entered.

STANDARDS ENTRY Page

- When **MEASURE STDS = YES**

  Use the up and down arrow keys to move up and down the list. When the highlight is on the field to be entered or edited press ENTER to display the Text Entry dialogue box. Enter the name of the Standard and press the ACCEPT function key when finished. The instrument returns to the STANDARDS ENTRY page with the concentration field for the standard highlighted. Press ENTER to display the edit dialogue box, enter the concentration using the numeric keypad, and press ENTER when finished. The instrument returns to the STANDARDS ENTRY page with the ID for the next standard highlighted.

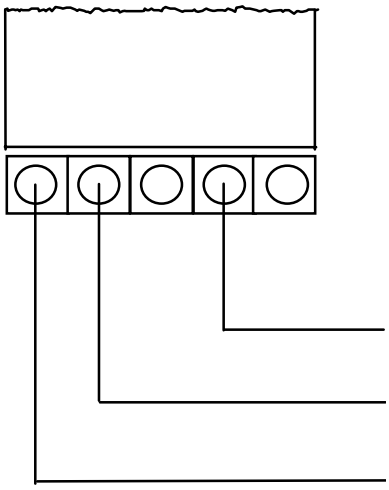
  Up to 20 standards can be entered in this way. The standards are displayed on two pages. The STD11 - STD20 function key toggles between the two pages.

- When **MEASURE STDS = NO**

  Press ENTER to display the LIBRARY page. Select and load the files for each standard in turn.

  A library of standards can be built up using the MULTI λ function in FIXED. The same method must be used for each MULTI λ result, and will be used for the MCA analysis.When the first MULTI λ file is loaded the current MCA method is changed to that used to obtain the MULTI λ result.

  Standards can thus be used in any combination without having to recalibrate for each new mixture.



STD1 - STD10/STD11 - STD20 - Toggles between displaying the first and second halves of the Standards List.

ACCEPT - transfers to the MCA METHODS page with the new list accepted.

CANCEL - Transfers to the MCA METHODS page leaving the old list unchanged.

WAVELENGTH ENTRY page

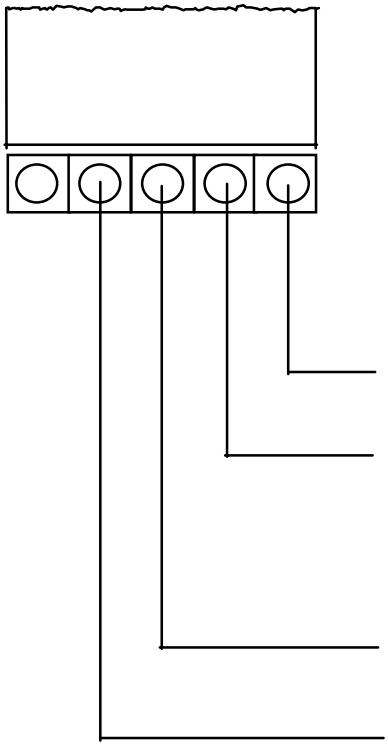
Use the up and down arrow arrow keys to move up and down the list. When the highlight is on the field to be entered or edited press ENTER to display the EDIT box and enter the values with the numeric keys. It is not necessary to enter the values in numerical order, although analysis will be quicker if they are. Press ENTER when finished. The instrument will return to the WAVELENGTH ENTRY page with the new value inserted in the list and the highlight moved to the next wavelength. When all wavelengths have been entered press the ACCEPT function key to return to the MCA methods page using the new list or the CANCEL function key to return leaving the old list unchanged.

Alternatively wavelengths may be entered directly from a scan. Clear the beam(s) and press ZERO BASE to perform a baseline scan, then put the sample in the cell holder and press the SCAN GRAPH function key. The instrument performs a scan using the method currently entered in the SCAN PARAMETERS page.

Use left and right arrow keys to move the vertical cursor to a suitable wavelength and press ENTER to mark it. Repeat until all required wavelengths have been marked. Marks can be removed using the CLEAR key, or the CLEAR ALL function key. When all required wavelengths have been marked press the ACCEPT function key to accept the list and return to the MCA Methods page.

Wavelengths can be selected either from a scan of the mixture to be analysed or by performing a scan on each standard in turn and selecting suitable wavelengths. Wavelengths already entered in the table are shown on the Scan Graph.

At least one wavelength must be entered for each standard.



ACCEPT - Transfers to the MCA METHODS page with all marked wavelengths added to the wavelength list.

FAST/SLOW - Toggles between two cursor speeds. In FAST mode the cursor jumps 5% of the graph or to the next data point whichever is the greater. In SLOW mode the cursor jumps to the next data point or the next display pixel whichever is the greater.

CLEAR ALL - Clears all marks.

RESCALE - Rescales the x and y-axes so that the spectrum fills the screen.

CALIBRATION

When the Standard Identifications and concentrations have been entered via the STANDARDS ENTRY page, and the wavelengths have been entered via the WAVELENGTH ENTRY page, the MCA application is ready for calibration.

Clear the beam(s) and press ZERO BASE to perform a baseline scan.

Press the CALIBRATE function key from the MCA METHODS page. If any results are present you will be given the option to proceed or cancel, with PROCEED highlighted.

All previous data will be lost if PROCEED is selected.

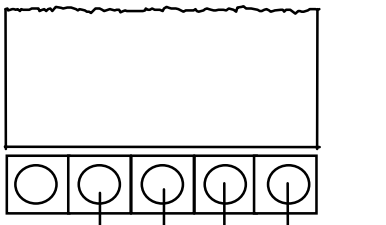
Press ENTER to proceed and then follow the on-screen prompts. Results for each standard will be stored in the Calibration Results Table with results for each standard on a new page. Use the up and down arrow keys to move between standards.

When the last calibration has been done put the first sample to be analysed in the beam and press RUN.

ANALYSING A SAMPLE

When a calibration has been performed or loaded with the method the MCA application is ready to use.

When RUN is pressed from the METHOD or RESULTS pages the instrument will measure the absorbance of the sample at each of the wavelengths specified in the method and compare with the absorbances of the standards at these wavelengths. The concentrations of each component are calculated and displayed on the results page. Results for each sample are displayed on a new page. Use the up and down arrow keys to move through the pages of results.



CLEAR RESULTS - Clears the results table.

MCA PAGE - Returns to the MCA METHOD page.

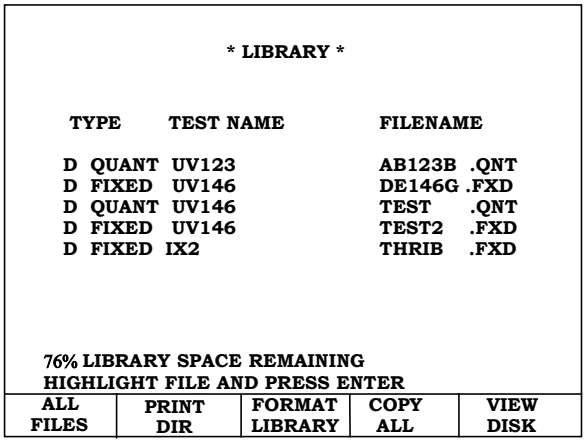
SAVE DATA - Displays the SAVE page from which the results can be saved to Library or Disk.

PRINT LIST - Prints the list on the selected printer

DATA STORE Pages

- To access the Data Store select the DATA STORE function key on the BIOMATE TESTS page.
- The Data Store page provides access to both the instrument Library and the disk drive. Both method and data files may be stored. The files can be loaded, renamed, copied to or from the disk drive, and deleted. Saving files to the Data Store is done from the method and result pages of the application.

LIBRARY Page



- The LIBRARY Page lists all the files in the Library, including the file type, description, and file name.

FILE TYPE

This describes the type of information contained in the file.

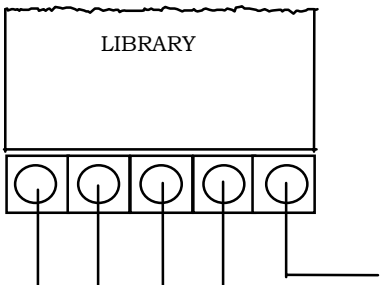
M BIO	BioMate test
D BIO	BioMate test and results
M SCAN	Scan method
D SCAN	Spectrum, data and method
M FIXED	Fixed wavelength method
D FIXED	Fixed wavelength results and method
M QUANT	Quant method, including calibration
D QUANT	Quant results, including method and calibration
M RATE	Rate method
D RATE	Rate graphics, data and method
M MCA	MCA method
D MCA	MCA results

TEST NAME

This is the description entered when the file was saved.

FILENAME

This is the DOS compatible filename used by the instrument and a computer.



VIEW DISK - Switches to the DISK page.

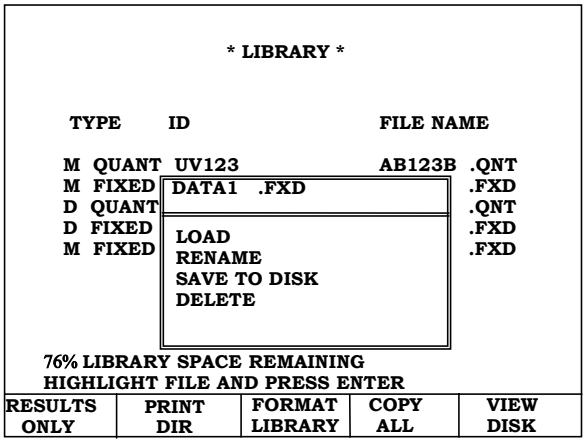
COPY ALL - Copies all files from Library to Disk

FORMAT LIBRARY - Clears all files from the library. *THIS WILL DELETE ALL THE FILES IN THE LIBRARY.*

PRINT DIR - Prints a list of all the files in the Library.

ALL FILES /RESULTS ONLY – Switches display between Methods + Results and Results only.

Using the Library



To perform an operation on a library file first select the file. To do this move the cursor to highlight the required file using the Up/Down Arrow keys.

If the file does not appear on the list the > and < arrow keys will scroll one page at a time down and up the list. There is a slight delay after the key is pressed while the next section of the directory is loaded. Once the required file is in the window, move the cursor to it using the Up/Down arrow keys as above.

With the required file highlighted, press ENTER to display the LIBRARY pop-up menu. Use the Up/Down arrow keys to highlight the required operation and press ENTER.

LOAD Loads the file from the Library

RENAME Switches to the SAVE/RENAME page where file name and description can be changed.

SAVE TO DISK Copies the highlighted file to the disk

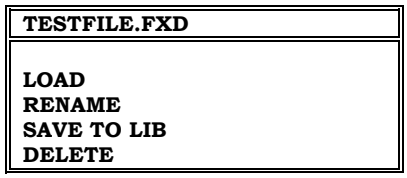
DELETE Removes the highlighted file from the library.

DISK Page

- This page allows access to the instrument disk drive. It lists all the files on the disk currently in the instrument drive, including file type, description and file name.

- Move the cursor to highlight the required file using the Up/Down Arrow keys.
  If the file does not appear on the list the > and < arrow keys will scroll one page at a time down and up the list. There is a slight delay after the key is pressed while the next section of the directory is loaded. Once the required file is in the window, move the cursor to it using the Up/Down arrow keys as above.

- When the required file is highlighted, select the file by pressing the ENTER key. The popup menu will appear. Then highlight the required operation and press ENTER.

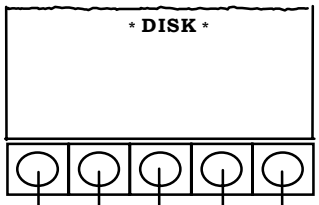


LOAD -Loads the file from Disk.

RENAME - Switches to the SAVE/RENAME page where file name and description can be changed.

SAVE TO LIB - Copies the highlighted file to the Library.

DELETE - Removes the highlighted file from the Disk.



VIEW LIBRARY – Switches to the LIBRARY page.

READ DISK - Reads the disk and refreshes the directory listing.

FORMAT DISK - Formats the disk as a 1.44 Mb disk. *THIS WILL DELETE ALL THE FILES ON THE DISK.*

PRINT DIR - Prints the list of files on the disk.

COPY ALL – Copies all method files from the Disk to the Library. *ENSURE THAT THE DISK CONTAINS ONLY VALID DATA OR METHOD FILES*

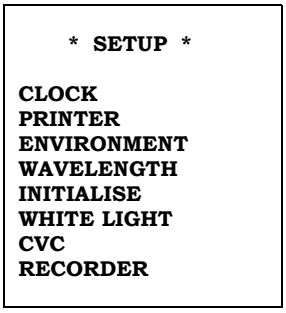
SETUP

Overview of Setup Options

- This section describes how to set up the instrument.
- The main system setup options are available directly from the SETUP function key on the BIOMATE TESTS or GENERAL TESTS pages.

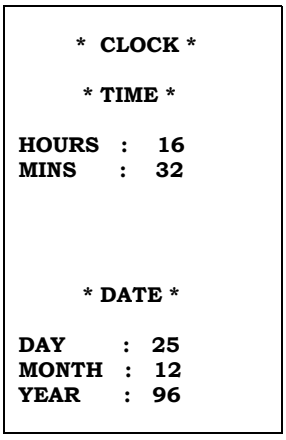
SETUP Page

- From the SETUP page move the cursor to the required option using the Up/Down Arrow keys. Select the option by pressing the ENTER key.



CLOCK : Switches to the CLOCK page.
PRINTER : Switches to the PRINTER page.
ENVIRONMENT : Switches to the ENVIRONMENT page.
WAVELENGTH : Switches to the WAVELENGTH CALIBRATION page.
INITIALISE : Switches to the OPTICAL INITIALISATION page.
WHITE LIGHT : Switches to the WHITE LIGHT Page.
CVC : Switches to the SETUP CVC Page.
RECORDER : Switches to the RECORDER Page.

CLOCK Page



- From this page the internal spectrophotometer clock/calendar can be reset.
- To reset the time or date highlight the required parameter and press ENTER. Enter the new value using the number keys and press ENTER.
- Once all the parameters have been changed press ACCEPT.

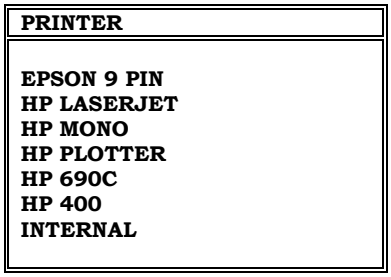
The date or time will not be changed unless ACCEPT is pressed.

- CANCEL cancels the edit, leaving the previous values unchanged

PRINTERS Page

- This page sets the system to work with the selected printer.

- The printer type is always highlighted. If an internal printer is supplied, this will be the default printer, otherwise the default printer is HP Mono.To choose a printer press ENTER to display the list of supported printers, and select using cursor keys. Press ENTER to confirm entry.



Printer options	Supported Printers
EPSON 9 PIN	Epson 9 or 24 Pin Dot Matrix, using ESC/P language.
HP LASERJET	HP Laserjet Series
HP MONO	HP Deskjet 500 Series (and above) - Black & White
HP PLOTTER	Compatible with plotters using HPGL language.
HP 690C	HP Deskjet 690C – Colour
HP 400	HP Deskjet 400 - Mono

- *Printers not on the above list that claim Epson 9 pin / 24 pin / ESC/P or HP PCL (Programming Control Language) Level 3 compatibility should work with the instrument but are not guaranteed to do so and are therefore not supported. If in doubt contact your local Thermo Spectronic approved Customer Support Organisation.*

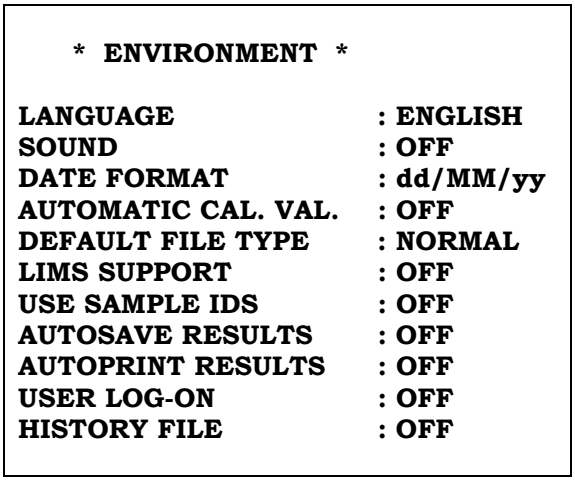
Note: Printers designed to work only in a Windows environment are not compatible with Local Control Software.

Before attempting to print using an external printer at any point during operation of the instrument, ensure that the printer is ready to print. Failure to do so will result in an error condition. Press CLEAR to clear the error message. Then rectify the problem with the printer, and try again.

ENVIRONMENT page

This page is used to select the language used for the software, the use of the beep, date format, and to enable/disable Automatic Calibration Validation and LIMS (Laboratory Information Management System) Support and to select the default filetype used when saving results. Where installed, UVCalc can be turned off from the Environment Page by pressing the UVCALC OFF function key.

When UVCalc has been turned off, the UVCalc disk will be required to reinstate it.


* ENVIRONMENT *
LANGUAGE : ENGLISH
SOUND : OFF
DATE FORMAT : dd/MM/yy
AUTOMATIC CAL. VAL. : OFF
DEFAULT FILE TYPE : NORMAL
LIMS SUPPORT : OFF
USE SAMPLE IDS : OFF
AUTOSAVE RESULTS : OFF
AUTOPRINT RESULTS : OFF
USER LOG-ON : OFF
HISTORY FILE : OFF

LANGUAGE : Select from the list. The language used immediately changes to the one selected.

SOUND : Turns the warning beeper ON or OFF. If set to OFF then the only indication of any error is the screen message.

DATE FORMAT: Defaults to dd/MM/yy, but will toggle with ENTER to MM/dd/yy.

AUTOMATIC CAL. VAL. : Toggles between OFF and ON with Enter.

- When ON, and the CVC (Calibration Validation Carousel) is fitted, the instrument automatically waits on start-up for the warm-up period (60 minutes) and then performs the Wavelength, Absorbance and UV Absorbance calibration tests (See CVC Section). Pressing Clear aborts the calibration.

DEFAULT FILE TYPE : Selects the default file type on the SAVE/RENAME page.

- Available formats are:

  NORMAL - The native file type used by the Local Control software
  CSV - Comma separated variable
  JCAMP-DX - JCAMP data exchange format

  Use up/down arrow keys to highlight choice and press ENTER to confirm selection.

LIMS SUPPORT : Toggles between **OFF** and **ON**.

- When **ON**, results, methods and sample IDs (when selected) are exported automatically after each measurement to the central LIMS computer via the RS232 port.

THIS INTERFACE MUST BE CONNECTED BEFORE LIMS SUPPORT IS ACTIVATED.

USE SAMPLE IDS **:** Choose between OFF, SEEDED and PROMPT USER.

- **OFF** - The system does not attach an identity to the sample.

- **SEEDED** - Enables the system to be set up to attach an identity to each sample automatically. This appears on the screen and the print-out. It is also exported to the LIMS (when enabled) with the results of the run and method used.

  Selection of **SEEDED** causes two additional items to appear in the Environment Menu:

  SAMPLE ID : Enter the name of the sample via the Text Entry Page.

  Use the Arrow keys to move the cursor to the required character and press ENTER. Once all the required characters (up to 11) have been entered press ACCEPT. If you make a mistake will act as a backspace or CLEAR will clear the whole entry.

  SAMPLE ID SEED : Sets the number to be used for the first sample, via the numeric keypad.

  The Sample ID is incremented automatically after each run.

- **PROMPT USER** - Before each run the Text Entry Page appears and the user is prompted to enter an identity for the sample.
  NOTE - a) When the 7 Cell Changer is used in automatic mode the Sample ID is incremented automatically without stopping for ID confirmation between samples.
  b) PROMPT USER is not compatible with the Sipper used in Sip and Run or AutoSampler modes

AUTOSAVE RESULTS **:** Toggles between ON and OFF.

When **ON,** results are saved automatically after each run. Selecting **ON** causes two additional items to appear in the Environment menu:

FILENAME - Enter a filename of up to 5 characters via the Text Entry Page.

FILE NUMBER - Enter a number between 0 and 999 via the numeric keypad. The number is appended to the filename and incremented automatically after each run.

AUTOPRINT RESULTS **:** Toggles between ON and OFF.

When **ON,** results are printed automatically after each run.

Before attempting to print at any point during operation of the instrument ensure that the printer is ready to print, ie switched on, on line and supplied with paper. Failure to do so will result in an error condition. Press Clear to clear the error message (the system may take a little time to respond). Ensure the printer is ready and retry.

USER LOG-ON : The default setting is OFF. Changing the setting to ON is password protected.

When set to **OFF,** any user has full access to all the functions of the instrument.
When set to **ON,** users must identify themselves by user name and password at log-on, and then have access to whichever functions are enabled for them by the System Administrator.

Setting User Log-on to ON is password protected. Use the up and down arrow keys to move the highlight to **USER LOG-ON** and press Enter. This brings up the Text Entry Page. When the correct password is entered USER LOG-ON is set to ON, otherwise an error message is displayed, and it remains set to OFF. The default password is ADMIN. Note that the password is case sensitive, and in this password all the letters are upper case.

Logging on as ADMIN gives access to the system at Administrator level, and the CHANGE USERS function key is enabled.

*** CURRENT USERS ***

NAME	PASSWORD	PRIVILEGES E	C	F	I	H	L	B
ADMIN	ADMIN	√	√	√	√	√	√	√
----------	----------	–	–	–	–	–	–	–
----------	----------	–	–	–	–	–	–	–
----------	----------	–	–	–	–	–	–	–
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----------	----------	–	–	–	–	–	–	–
----------	----------	–	–	–	–	–	–	–

E = EDIT METHODS
C = CALIBRATIONS
F = DELETE FILES
I = INITIALISATIONS
H = HISTORY FILE
L = RESET LIFETIMES
B = DEFAULT BASELINE

CANCEL	ACCEPT		USERS 11 - 20	

Pressing the CHANGE USERS function key brings up the CURRENT USERS page. Up to 20 users can be listed by name and password. The privileges of each user can be set individually by the Administrator, and can be any combination of Edit Methods, Calibrations, Delete Files, Initialisations, History File, Reset Lifetimes, Default Baseline.

Only the Administrator is able to change passwords or edit the Current Users Page. It is strongly recommended that a new password for the Administrator is set as soon as USER LOG-ON is activated, and that USER LOG-ON is activated whenever the instrument is to be used in a multi-user environment.

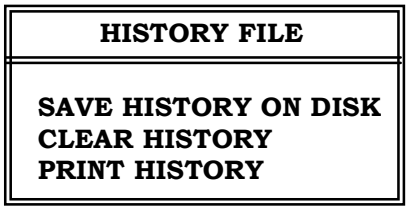
After USER LOG-ON is enabled, each time the instrument is powered up the user will be prompted to log on by entering name and password. At the close of a session the user logs off by pressing the LOG OFF function key on the General Tests and Setup Pages, and choosing whether to PROCEED or STOP. When PROCEED is chosen the system waits for the next user to enter their name.

USER LOG-ON can be reset to OFF only by the Administrator. After USER LOG-ON has been set to OFF the list of users is cleared and the default User Name and Password are both reset to ADMIN.

HISTORY FILE **:** Toggles between ON and OFF.

The History File contains the history of the instrument. An entry is put into the file when there are changes to default baselines, wavelength calibrations, EHT calibrations, sipper calibrations and CVU tests, noting date, time and user. The file will also contain records of operations carried out by engineers during maintenance visits.

When **HISTORY FILE** is set to ON the HISTORY FILE function key becomes available on the Environment Page, unless USER LOG-ON is enabled and the user has been denied access by the Administrator. Pressing this function key brings up the History File Pop-up box.



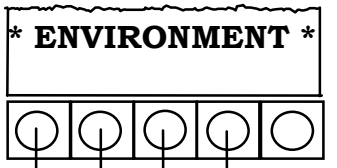
SAVE HISTORY ON DISK - The user is prompted for a file name and the instrument history is saved in CSV format which may be read by a suitable spreadsheet or text editor.

CLEAR HISTORY - Clears the Instrument History.

PRINT HISTORY - The Instrument History is printed out.

Make sure the printer is connected and ready before selecting PRINT HISTORY.

The History File contains a maximum of 400 entries. When the number of entries reaches 390 a warning message is displayed, and it is necessary for the Administrator or a user with the History File privilege save to disk and/or print the existing history file, then clear the history file to make room for more entries.



HISTORY FILE - Appears when History File is enabled.

CHANGE USERS - Available only to Administrator when User Log-on enabled.

UVCALC OFF *- Only appears when UVCalc has been installed. Disables UVCalc and re-enables functions that UVCalc disables.

SETUP PAGE - Returns to the SETUP page.

** When UVCalc has been turned off, the UVCalc disk will be required to reinstate it.*

WAVELENGTH CALIBRATION Page

*** WAVELENGTH CALIBRATION ***
CALIBRATION : USING D2 LAMP

- From this page the Wavelength calibration of the instrument can be adjusted.

WARNING: DO NOT ATTEMPT TO RECALIBRATE THE INSTRUMENT UNLESS YOU ARE ABSOLUTELY SURE YOU NEED TO DO SO. IF IN ANY DOUBT CONTACT THERMO SPECTRONIC APPROVED CUSTOMER SUPPORT.

ENSURE BOTH SAMPLE AND REFERENCE BEAMS ARE CLEAR BEFORE ATTEMPTING ANY WAVELENGTH CALIBRATION.

- This option will optimise the wavelength calibration of the instrument by measuring the Deuterium lamp emission line at 656.1nm and fitting the calibration accordingly. It should only be attempted if for any reason the instrument no longer achieves its quoted wavelength accuracy specification.

The calibration will take at least 10 minutes.

- Ensure Deuterium Lamp is ON.
- Ensure instrument is fully warmed up and the beams are clear.
- From WAVELENGTH CALIBRATION page press CALIBRATE.
- Once calibration is complete switch the instrument OFF.
- Switch instrument and Deuterium lamp ON and allow to warm up.
- Run Default Baseline.

OPTICAL INITIALISATION Page

- This page is used to reset the instrument and define its initialisation and default baseline. These procedures ensure the optimum performance of the spectrophotometer.

INITIALISATION TYPE : When selected this displays a pop-up menu to choose between initialisation of optics or baseline.

OPTICS - During initialisation the instrument performs some simple hardware checks, calculates various data tables and measures the dark current. The filter wheel is then initialised before the instrument drives to the default wavelength and performs an autozero.

BASELINE - This re-measures the default baseline. Ensure that both lamps are on and that the spectrophotometer is fully warmed up. This process will take about one hour.

The default baseline should be re-measured whenever one of the source lamps is changed or if the instrument is working at temperatures significantly different from 25 °C, or if the wavelength calibration is altered.

INITIALISE WITH D2 : This sets the instrument to initialise with or without the Deuterium lamp on. If set to ON then the instrument will automatically strike the Deuterium lamp during initialisation.

WHITE LIGHT Page

- The **WHITE LIGHT** feature is used to facilitate alignment of optical accessories in the sample compartment.
- When the **INITIALISE** function key is pressed the instrument will align the grating so that the zero order diffraction passes through the sample compartment. This provides a beam of white light which can be seen when a white card or similar is placed in the light path. In double beam instruments the action of the chopper causes the light to alternate between the sample and reference beams.
- When alignment is completed, pressing the **STOP** function key returns the grating to its normal position and pressing the **SETUP PAGE** function key returns to the Setup Page.

SET UP CVC Page

- This page allows the CVC calibration data (provided on disk) to be loaded into the spectrophotometer memory. For full details please see the CVC section of this manual.

RECORDER Page

```
        * RECORDER *

CHART HIGH (ABS)          : 3.000
CHART LOW (ABS)           : -0.300

CHART HIGH (%T)           : 200.0
CHART LOW (%T)            : 0.1

CHART HIGH (I)            : 99.9999
CHART LOW (I)             : 0.0000
```

- The Chart High and Chart Low parameters set the full scale deflection on the analogue chart recorder output for each of the available measurement modes. On startup, these limits are set to the maximum measurement ranges (as shown above).
- To reset the limits highlight the required parameter and press ENTER. Enter the new value using the number keys and press ENTER.

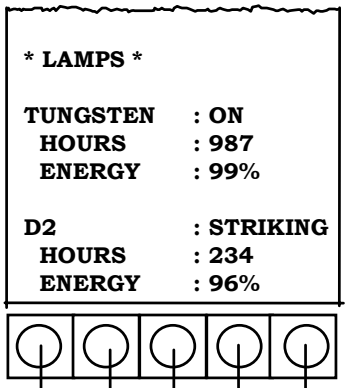
Using a Chart Recorder

- Use the Recorder Lead (part number 4401 172 00401) to connect the recorder to the socket labelled REC located to the rear of the spectrophotometer. This lead is used for both 0-10mV and 0-1V full scale deflection (fsd) chart recorders. Use the blue plug for 0-10mV, or the red plug for 0-1V.
- N.B. If your chart recorder is capable of either voltage range, it is advisable to use the 0-1V setting and only use the 2 appropriate plugs (red and black).
- The Chart High and Chart Low parameters set the 0 to 1V full scale deflection (fsd) on the analogue chart recorder output for each of the available measurement modes.
- Operating tip: if you are working with absorbances close to zero best results are obtained if the Chart Low (ABS) limit is set to a small negative value, say -0.1A.
- Now navigate to your chosen method, insert a blank sample and press ZERO. Once the instrument has finished zeroing, adjust the chart recorder backoff so that its baseline is at the required position.
- N.B. The chart recorder will be driven off scale while the instrument is zeroing.

LAMPS Page

- The lamp functions are available directly from the LAMPS key on the SETUP page. If User Log-on is not in use, the GENERAL TESTS page will also have a LAMPS key.
- This page shows the status of the Tungsten Halogen and Deuterium lamps whether ON, OFF or FAILED, and their appropriate energy levels. It also allows the lamp hours to be reset and the Deuterium lamp to be switched on or off.
- The HOURS parameter states the number of hours that the lamp has been in use.

The Tungsten Halogen lamp should be replaced after 2000 hours. The Deuterium lamp should be replaced after 1000 hours.
Whenever a lamp is changed then the hours parameter should be reset to zero.



RESET W HRS - Resets hours and measures energy at the appropriate wavelength. **ALLOW THE LAMP AT LEAST 10 MINUTES TO WARM UP BEFORE RESETTING ITS HOURS.**

RESET D2 HRS - Resets hours and measures energy at the appropriate wavelength. **ALLOW THE LAMP AT LEAST 10 MINUTES TO WARM UP BEFORE RESETTING ITS HOURS.**

W ENERGY - **ALLOW THE LAMP AT LEAST 10 MINUTES TO WARM UP BEFORE MEASURING ITS ENERGY. CLEAR BOTH SAMPLE AND REFERENCE BEAMS BEFORE MEASURING LAMP ENERGIES.**

W ENERGY - **ALLOW THE LAMP AT LEAST 10 MINUTES TO WARM UP BEFORE MEASURING ITS ENERGY. CLEAR BOTH SAMPLE AND REFERENCE BEAMS BEFORE MEASURING LAMP ENERGIES.**

SWITCH D2 -Turns the Deuterium lamp ON or OFF depending on its current status.

7 CELL CHANGER

- The 7 Cell Changer is fitted as standard and enables up to seven samples to be presented for measurement sequentially.
- This section describes the operation of the accessory with the software and also describes its removal / refit.

When the 7 Cell Changer is installed then a status box appears on the top right hand side of the screen, to the left of the Absorbance/Wavelength box, indicating the the presence of the accessory and its setting.

If this status box is displayed, then the 7 Cell Changer can be moved manually using the < > arrow keys. To step foward/backward many positions, repeated pressing of the key will be 'remembered' by the system.

```
        * CELL   CHANGER *

CELL POS.          : 1
SPEED              : HIGH
```

- This page allows the 7 Cell Changer to be set up. To reach this page press ACCESSORIES from the GENERAL TESTS or SETUP pages then select CELL CHANGER and press ENTER.

CELL POS. **:** Used to change the current cell position. This change is reflected in the Status box.

SPEED **:** Displays a pop-up list to enable HIGH, MEDIUM or LOW rotation speed to be selected.

FUNCTION KEY

INITIALISE Resets the accessory and places cell 1 in the sample beam.

7 CELL CHANGER - REMOVAL AND REFIT

This procedure is essential for the fitting of any of the alternative cell holders available for long pathlength cells, single cell thermostatting, or the MiniSipper.

If the 7 Cell Changer basket is removed / replaced at any time, the 'Refit' procedure must always be repeated.

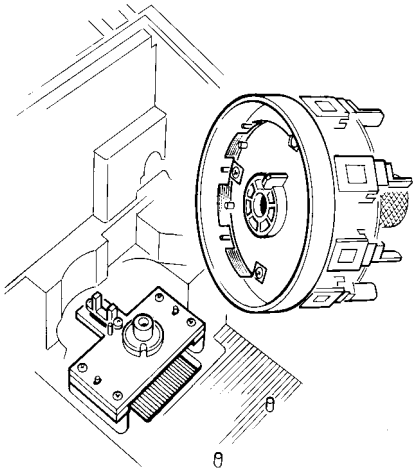
REMOVAL:

- Holding the basket firmly with one hand, unscrew the central screw anti-clockwise until the basket is released.
- **REPLACE THE COVER ON THE OPTOSENSOR**, and secure the cell holder.

REFIT:

- Remove the cover from the optosensor, and remove the cell holder.
- Indentify the position of the ‘keyway’ on the motor shaft.
- View the underside of the basket to locate the position of the moulded ‘key’.
- Re-locate the basket on the shaft ensuring a positive location of the key in the keyway, and tightened the central screw clockwise.
- **From the CELL CHANGER page use the INITIALISE function key to correctly align the basket with the spectrophotometer.**

This last action is important to ensure the correct operation of the system. Whilst there is significant resistance to manual movement of the motor, it is suggested that ‘as routine’ initialisation of the 7 Cell Changer should be performed as a check before any measurements are performed.



SUPERSIPPER

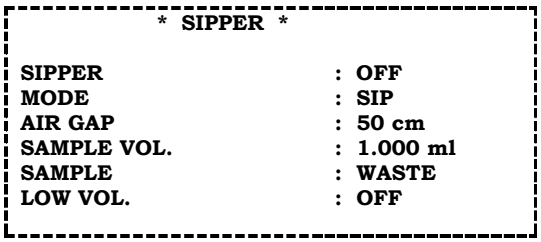
- The SuperSipper is an optional accessory that enables samples to be drawn into a flowcell of the user's choice for automatic measurement. After the measurement is complete the sample may be sent to waste or returned to its original vessel. A continuous pumping mode allows the system to be washed through when required, e.g. between applications.

- This section describes the operation of the SuperSipper with the Local Control software. Full details of the installation and operation of the accessory are described in the SuperSipper Installation and Maintenance Manual (9499 230 29611) supplied with the SuperSipper.

- To operate the SuperSipper, install as described in the above manual. Present the sample to the SuperSipper and press the switch. The required sample volume will be drawn into the tubing. When the system beeps remove the sample and the required air gap will be drawn in. Once the measurement has taken place press the switch again. The sample will be pumped out of the flowcell either to waste or returned to the sample vessel.

When the sipper is connected a status box is displayed on the right hand side of all the method screens that indicates the presence of the SuperSipper and its status.

SIPPER Page



- This page allows the SuperSipper to be set up for the required analysis. The method set on this page will be saved with any data produced by the software.

- To reach this page press the ACCESSORIES function key on the SETUP or GENERAL TESTS page then select SIPPER and press ENTER.

To change a parameter highlight the required value using the Up/Down Arrow keys and press ENTER.

SIPPER **:** Selects from ON, OFF or STANDBY.

In STANDBY mode, the sipper pumps a small volume approximately every 30 minutes. This is to change the point at which pressure is applied to the Sipper tubing, thus preventing the formation of a permanent kink. The first 6 movements are in the Return direction, and the next 6 are in the Waste direction. The total volume pumped is sufficiently small as to ensure that any sample present remains in the tubing. When the sipper is operated normally, its clock is reset and the Standby process re-starts.

MODE **:** Selects from SIP / SIP&RUN / CONTINUOUS / AUTOSAM.

SIP Sets the system to fill the flowcell. If SAMPLE is set to RETURN then alternate switch presses will fill and empty the flowcell. In this mode instrument operation is completely independent of the SuperSipper

SIP&RUN Sets the system to fill the flowcell and automatically perform a measurement. If SAMPLE is set to RETURN then alternate switch presses will fill and empty the flowcell. The current method used to produce the result (e.g. if FIXED is current then the sample will be measured using the FIXED METHOD as set).

CONTINUOUS Sets the system to pump continuously to waste. Alternate switch presses will start and stop pumping. In this mode instrument operation is completely independent of the SuperSipper.

AUTOSAM Sets the system to work with the Gilson 221XL and 222XL Autosamplers. Refer to the Autosampler Interface manual for further details.

AIR GAP **:** Enter value between 0 and 500 cm.

Sets the gap between the trailing meniscus of the current sample and the leading meniscus of the next sample. The gap is measured to the nearest centimetre.

For best results set the airgap no less than 8cm from the flowcell.

SAMPLE VOL **:** Enter a value between 0.2 and 9.999 ml.

Sets the volume of sample to be pumped.

SAMPLE **:** Selects from WASTE or RETURN.

WASTE After measurement the sample is pumped through the flowcell to waste by the act of pumping the next sample.

RETURN After measurement the pump direction is reversed and the sample is returned to the sample vessel.

LOW VOL **:** Toggles ON or OFF.

Automatically adjusts the pumping time to maintain the correct air gap for narrow uptake tubing.

OFF Use standard internal diameter (1.1mm) uptake tube.

ON Use narrow internal diameter (0.8mm) uptake tube

FUNCTION KEYS

VIEW CALIB Goes to the SIPPER CALIBRATION page.

CALIBRATE Starts the Sipper calibration procedure.

Sipper Calibration

- This calibrates the SuperSipper to take account of variations in pump and uptake tubing and sample viscosities. A volume is set and using the appropriate solvent and tubing several sips are performed. The actual volume sipped is entered and a calculation done to produce a calibration factor. This factor is then used to adjust the pumping time to ensure that the correct volume of sample is always used.
- Details of the calibration used are displayed on the SIPPER CALIBRATION page.

CALIBRATE SIPPER Page

```
     * CALIBRATE   SIPPER *


NOMINAL VOL.       : 1.000 ml
NO. SIPS DONE      : 5
```

- Using the solvent and tubing which will be used for the sample solutions offer a measuring cylinder filled to the highest gradation to the sipper uptake tube and press the switch plate.

The sipper will pump a sample and the spectrophotometer will issue a beep. Withdraw the measuring cylinder and the sipper will pump the air gap. The values used for sample volume and air gap are those set on the SIPPER page.

- Repeat this process for a number of cycles up to a maximum of 10 then press ENTER.
- Measure the total volume taken from the measuring cylinder and enter this. The calibration will be displayed.

FUNCTION KEY

SIPPER PAGE	Returns to the SIPPER page and abandons the calibration.

SIPPER CALIBRATION Page

```
          * SIPPER   CALIBRATION *
          25/10/96   16:47

NOMINAL VOL.          : 1.000 ml
NO. SIPS DONE         : 5
TOTAL VOL SIPPED      : 5.100 ml
TUBING CAL            : 1.020
```

- This page displays the current sipper calibration.
- To alter the calibration, press CALIBRATE

FUNCTION KEYS

SIPPER PAGE	Returns to the SIPPER page.
CALIBRATE	Starts the calibration procedure.

MINISIPPER

- The MiniSipper is an optional accessory that enables samples to be drawn into a flowcell of the user's choice for automatic measurement. After the measurement is complete the sample is sent to Waste. A continuous pumping mode allows the system to be washed through when required, e.g. between applications.

- This section describes the operation of the MiniSipper with the Local Control software. Full details of the installation and operation of the accessory are described in the MiniSipper Installation and Maintenance Manual (9499 230 45111) supplied with the MiniSipper.

- To operate the MiniSipper install as described in the above manual. Present the sample to the MiniSipper and press the switch. The required sample volume will be drawn into the tubing. When the system beeps remove the sample and the required air gap will be drawn in. Once the measurement has taken place press the switch again. The sample will be pumped out of the flowcell to waste.

When the sipper is connected a status box is displayed on the right hand side of all the method screens that indicates the presence of the MiniSipper and its status.

SIPPER Page

```
        * SIPPER *

SIPPER              : OFF
MODE                : SIP
AIR GAP             : 50 cm
SAMPLE VOL.         : 1.000 ml
SAMPLE              : WASTE
LOW VOL.            : OFF
```

- This page allows the MiniSipper to be set up for the required analysis. The method set on this page will be saved with any data produced by the software.

- To reach this page press the ACCESSORIES function key on the SETUP or GENERAL TESTS page then select SIPPER and press ENTER.

To change a parameter highlight the required value using the Up/Down Arrow keys and press ENTER.

SIPPER **:** Toggle ON or OFF.
Switches the MiniSipper ON or OFF.

MODE **:** Selects from SIP / SIP&RUN / CONTINUOUS.

SIP Sets the system to fill the flowcell.

SIP&RUN Sets the system to fill the flowcell and automatically perform a measurement. The current method is used to produce the result (e.g. if FIXED is current then the sample will be scanned using the FIXED METHOD as set).

CONTINUOUS Sets the system to pump continuously to waste. Alternate switch presses will start and stop pumping. The instrument will not process any key presses while the MiniSipper is pumping in continuous mode.

AIR GAP **:** Enter value between 0 and 500 cm.

Sets the gap between the trailing meniscus of the current sample and the leading meniscus of the next sample. The gap is measured to the nearest centimetre.

For best results set the airgap no less than 8cm from the flowcell.

SAMPLE VOL **:** Enter a value between 0.5 and 9.999 ml.

Sets the volume of sample to be pumped.

SAMPLE **:** Set to WASTE.

After measurement the sample is pumped through the flowcell to waste by the act of pumping the next sample.

LOW VOL **:** Set to OFF.

A standard internal diameter (4.0mm) uptake tube is used.

FUNCTION KEYS

VIEW CALIB Goes to the SIPPER CALIBRATION page.

CALIBRATE Starts the Sipper calibration procedure.

Sipper Calibration

- This calibrates the MiniSipper to take account of variations in pump and uptake tubing and sample viscosities. A volume is set and several sips are performed using the appropriate solvent. The actual volume sipped is entered and a calculation done to produce a calibration factor. This factor is then used to adjust the pumping time to ensure that the correct volume of sample is always used.
- Details of the calibration used are displayed on the SIPPER CALIBRATION page.

CALIBRATE SIPPER Page

```
      * CALIBRATE   SIPPER *

NOMINAL VOL.        : 1.000 ml
NO. SIPS DONE       : 5
```

- Using the solvent which will be used for the sample solutions, offer a measuring cylinder filled to the highest gradation to the sipper uptake tube and press the switch.

The sipper will pump a sample and the spectrophotometer will issue a beep. Withdraw the measuring cylinder and the sipper will pump the air gap. The values used for sample volume and air gap are those set on the SIPPER page.

- Repeat this process for a number of cycles up to a maximum of 10 then press ENTER.
- Measure the total volume taken from the measuring cylinder and enter this. The calibration will be displayed.

FUNCTION KEY

SIPPER PAGE Returns to the SIPPER page and abandons the calibration.

SIPPER CALIBRATION Page

```
          * SIPPER    CALIBRATION *
          25/08/99    16:47

NOMINAL VOL.          : 1.000 ml
NO. SIPS DONE         : 5
TOTAL VOL SIPPED      : 5.100 ml
TUBING CAL            : 1.020
```

- This page displays the current sipper calibration.
- To alter the calibration press CALIBRATE

FUNCTION KEYS

SIPPER PAGE	Returns to the SIPPER page.
CALIBRATE	Starts the calibration procedure.

CALIBRATION VALIDATION CAROUSEL (CVC)

- The Calibration Validation Carousel replaces the standard cell basket, and allows for the automatic checking of the spectrophotometer to specification, by measurement of the fundamental operating parameters.

THE PROCESS OF CALIBRATION OF ITS WAVELENGTH AND ABSORBANCE FILTERS IS ACCREDITED BY THE UNITED KINGDOM ACCREDITATION SERVICE (UKAS) TO AN ISO/IEC GUIDE 25 APPROVED PROCEDURE.

- Calibration can be performed automatically on start-up if the CVC is fitted. From the SETUP menu select ENVIRONMENT, select AUTOMATIC CAL. VAL. and toggle to ON with the Enter key. On start-up the instrument will then automatically wait for the warm-up period (60 minutes) and then perform tests 1,2 and 3. Calibration can be aborted by pressing Clear.

- Calibration values are provided on a PC format floppy disk, which is loaded on installation (see below).

IT IS RECOMMENDED THAT A BACK-UP COPY OF THIS DISK IS MADE BEFORE USE, AND THE MASTER RETAINED IN A SECURE SAFE LOCATION.

- This section describes the installation and operation of the accessory with the software.

- This section also describes its removal / refit.

SETUP CVC

```
          * SETUP    CVC *

CALIBRATION DATA

   SERIAL NUMBER        : 32764
   CALIBRATION DATE     : 03/12/96

CAROUSEL
    SERIAL NUMBER       : 32764
```

- This page allows the CVC calibration data (provided on disk) to be loaded into the spectrophotometer memory. To reach this page highlight the CVC option from the SETUP page, and press ENTER.

CALIBRATION DATA

SERIAL NO. : Displays the serial number of the calibration, and therefore the actual parameter values loaded into the memory of the spectrophotometer.

CALIBRATION DATE : Date of original calibration.

CAROUSEL SERIAL NO. : Unique identifier read by initialising the carousel.

FUNCTION KEYS

LOAD DATA	Allows calibration data to be loaded into the spectrophotometer.
INITIALISE	Initialises the carousel, and reads the serial number.
SETUP PAGE	Returns back to SETUP.

SETUP PROCEDURE

- From SETUP, choose CVC, and place the disk in the drive on the spectrophotometer.

The first time this procedure is actioned, a warning message 'W1022 -NVM Checksum' will be displayed. This is expected. Press 'C' to clear.

- With the disk in place, press LOAD DATA. Appearance of the appropriate Serial Number and Calibration Date confirms storage of the data in NVM.

CAROUSEL INSTALLATION

- Remove the cover from the optosensor.
- Identify the position of the 'keyway' on the motor shaft.
- View the underside of the basket to locate the position of the moulded 'key'.
- Re-locate the basket on the shaft ensuring a positive location of the key in the keyway, and tightened the central screw clockwise.
- **From the CVC page use the INITIALISE function key to correctly identify the carousel with the spectrophotometer.**

At this point check that the two serial numbers match.

CVC HOME Page

*** CVC TEST ***

TEST	STATUS	TIME	DATE
1. WAVELENGTH	PASS	11 : 05	03/12/96
2. ABSORBANCE	PASS	11 : 20	03/12/96
3. UV ABSORBANCE	PASS	11 : 25	03/12/96
4. STRAY LIGHT	PASS	11 : 28	03/12/96
5. BANDWIDTH	PASS	11 : 33	03/12/96
6. NOISE	PASS	11 : 38	03/12/96
7. DRIFT	PASS	12 : 40	03/12/96

- This page is reached by pressing CAL. VAL. from the General Tests page.
- This page lists the available tests and for each test reports the time and date on which the last test was run and whether it passed or failed.
- To perform a test highlight the required option(s) either individually using the Arrow keys or as a group using the appropriate function keys and press RUN.

The instrument and lamp hours and lamp energies are calculated and displayed on the appropriate page as each test is run.

FUNCTION KEYS

SAVE RESULTS	Goes to the SAVE page from where the current set of results can be saved to Library or Disk. Files are saved with a .TST extension.
PRINT SUMMARY	Prints the summary of results as shown on the page.

PRINT ALL	Prints the summary of results as shown on the page and full details of the results of each of the tests.
TESTS 1-3	Selects the first three tests in the list. These will be run in sequence when RUN is pressed.
ALL TESTS	Selects all the tests in the list. These will be run in sequence when RUN is pressed.

Every time a test is run, the carousel serial number is read and recorded on the results. If this does not match the Calibration Data, then the error E3083 - "Serial Numbers do not match" is reported.

RESULTS Pages

- Each results page fully details:

- the test performed.
- the actual, and measured values.
- the differences, tolerances, etc. (as appropriate).
- the spectrophotometer and CVC serial numbers.
- the instrument hours, lamp hours and lamp energies.

From each Test Page the following functions are available.

FUNCTION KEYS

TEST PAGE	Returns to the TEST HOME page.
SAVE RESULTS	Goes to the SAVE page from where the results can be saved to Disk.
PRINT RESULT	Prints the result of the test.
STOP	Stops a test. Only present whilst a test is running. If STOP is pressed then any results obtained from a test up to that point are discarded.

CVC - REMOVAL AND REFIT

REMOVAL:

- Holding the basket firmly with one hand, unscrew the central screw anti-clockwise until the carousel is released.
- Replace the CVC (as soon as convenient) in its protective storage box.
- **REPLACE THE COVER ON THE OPTOSENSOR,** unless the 7 Cell Changer is to be fitted.

REFIT:

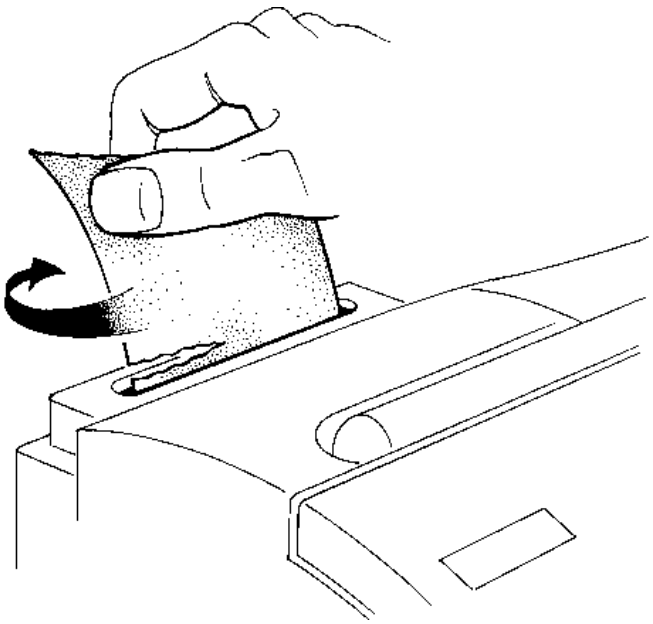
- Remove the cover from the optosensor.
- Identify the position of the 'keyway' on the motor shaft.
- View the underside of the basket to locate the position of the moulded 'key'.

- Re-locate the basket on the shaft ensuring a positive location of the key in the keyway, and tightened the central screw clockwise.

- **From the CVC page use the INITIALISE function key to correctly identify the carousel with the spectrophotometer.**

This last action is important to ensure the correct operation of the system. Whilst the spectrophotometer will check for data to carousel match on running any test, an initial confirmation is recommended.

INTERNAL PRINTER



- The Internal Printer is a factory-fitted thermal-head printer. It is supplied with a roll of 11.2cm wide single-ply thermal paper. Paper rolls may be ordered separately under the following part number: 4401 161 00391
- For long-term storage, it is recommended that the paper is kept away from light and at room temperature.
- A red warning stripe is printed on the paper within 1 metre of the end of the roll. It is recommended that the roll is replaced as soon as the warning stripe is visible to avoid possible paper jams.
- The printer is fitted with a Line Feed Button. Press this once to switch the printer off-line and feed the paper though the printer. Press the button a second time to put the printer back on-line. Do not press the Line Feed Button during printing as this will cause a internal error condition which can only be rectified by restarting the instrument.

To replace the paper roll:

- Cut the paper at the end of the new roll in a “V” to make a point at the end of the paper.
- Carefully feed the printer paper (from the bottom of the roll, i.e. shiny side down) into the back of the printer using the Line Feed Button.
- Keep the Line Feed Button depressed until the paper emerges “squarely” through the top slot of the printer housing.

MAINTENANCE

- The information given in this section deals only with those parts of maintenance or service which can be safely carried out by the user. Work other than that detailed should be carried out by a service engineer.

- **ALWAYS ENSURE THAT BOTH THE SAMPLE AND REFERENCE BEAMS ARE CLEAR BEFORE SWITCHING ON THE INSTRUMENT. Failure to do so will produce abnormal results.**

- Low lamp energy values can be caused by leaving cells in the sample and/or reference beams during energy measurement. **ALWAYS CHECK THAT BOTH BEAMS ARE CLEAR BEFORE MEASURING LAMP ENERGIES.**

- Abnormal results will be produced if a sample is left in the beam when ZERO/BASE is pressed. **ALWAYS ENSURE THAT THE SAMPLE IS REMOVED AND THAT BOTH BEAMS ARE CLEAR OR CONTAIN THE APPROPRIATE ZERO REFERENCES BEFORE ZEROING THE INSTRUMENT OR PERFORMING A BASELINE SCAN.**

- **VERY OFTEN POOR INSTRUMENT PERFORMANCE OR FAILURE CAN BE ATTRIBUTED TO SIMPLE FAILURE OF THE TUNGSTEN LAMP - THEREFORE REPLACE (AS BELOW) USING THE SPARE LAMP PROVIDED BEFORE SEEKING FURTHER ASSISTANCE.**

- If any fault occurs (including the above lamp failure), these are reported by the system as an ‘Error condition’, and an ‘Exxxx’ number is generated. Descriptive text is also included with this message.

  DETAILED BELOW ARE THE ERROR CODES PRODUCED IF:

  1. The tungsten lamp fails or is poorly aligned
     E3010 E3011 E3104 E3015 E3030

  2. The deuterium lamp fails
     E3003 E3004 E3005 E3006 E3007 E3008 E3009 E3012 E3013 E3022 E3029 E3044 E3045

  3. The beam(s) is blocked on initialisation
     E3027 E3056

  4. The 7 Cell Changer is stalled in use (or fails to initialise)
     E3001 E3002 E3054 E3055 E3082 E3084

  5. The sample compartment is open
     E3053 E3062 E3068 E3069 E3071

- A comprehensive list of these codes is available in the Service Manual for this product. Generation of a code not related to replacement of either the tungsten or deuterium lamps usually requires you to contact your local Thermo Spectronic approved Customer Support Organisation.

ROUTINE MAINTENANCE

Very little maintenance is required to keep the spectrophotometer in good working condition. The interior should be kept as dust free as possible and the sample compartment cleaned regularly; wipe off spilt chemicals immediately.

Replacement sample compartment liners are available under the following part number:
9423 UV9 7020E

Cleaning Instrument Exterior

The exterior of the instrument can be cleaned periodically as follows:

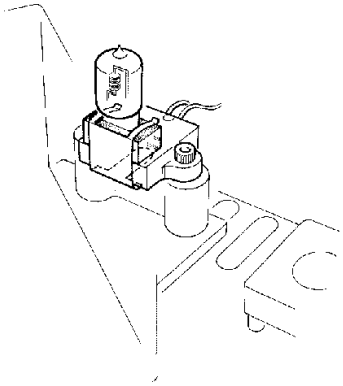
CAUTION: Do not allow moisture to leak into the instrument.

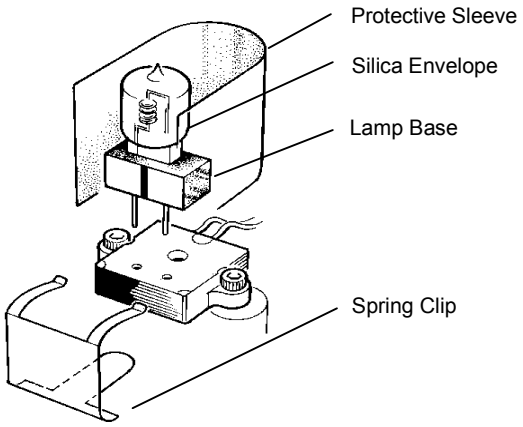
- Switch off the spectrophotometer and disconnect from the mains supply.
- Using a lint free cloth dampened with a weak solution of detergent and water, wipe the exterior surface of the instrument as necessary.
- Wipe over with a cloth dampened with plain water.
- Dry the surface with another cloth.

REMOVAL AND REPLACEMENT OF TUNGSTEN HALOGEN LAMP

WARNING: Switch off and disconnect the spectrophotometer from the mains and allow the lamp to cool for at least 15 minutes before proceeding.

- Remove the back corner cover by turning the fastener one quarter turn anti-clockwise and slide the cover up to remove.
- Now lift the metal lamp cover vertically upwards to remove it.





- If fitted, remove the spring clip
- Hold the Tungsten lamp and pull upwards to remove.

When fitting the new tungsten halogen lamp, avoid handling the silica envelope. Finger marks become burnt on and cannot be removed after the lamp is switched on. As this can affect the output characteristics, handle only the base of the lamp. If the silica envelope does become contaminated, clean with a powerful degreasing solvent such as absolute alcohol before the lamp is switched on.

- Use the new lamp's protective sleeve, a polythene bag or a piece of tissue paper wrapped around the lamp and insert the pins into the socket.
- Replace the spring clip.

These lamps are manufactured to very high tolerances, but to ensure optimum energy throughput, align the lamp filament exactly as shown in the diagram, with the white line on the lamp base facing towards the front of the instrument.

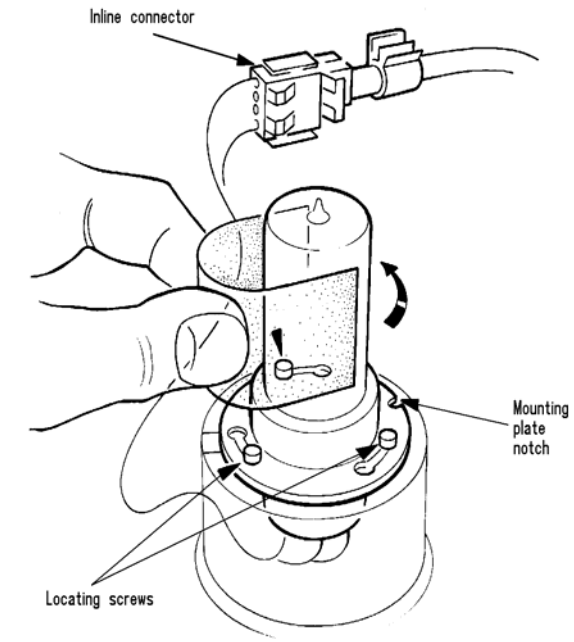
- Refit both the metal lamp cover and the rear cover.
- Reconnect the spectrophotometer to the mains supply and switch on.
- Lamp hours and energy must be reset from the controlling software.

REMOVAL AND REPLACEMENT OF DEUTERIUM LAMP

WARNING: (1) Switch off and disconnect the spectrophotometer from the mains supply and allow the lamp to cool for at least 15 minutes before proceeding.

(2) UV radiation from a Deuterium lamp can be harmful to the skin and eyes. Always view the lamp through protective glasses that will absorb UV radiation. Avoid looking directly at the Deuterium arc. Do not expose the skin to direct or reflected UV radiation.

- ❑ Set the power switch to off and disconnect the spectrophotometer from the mains supply.
- ❑ Remove the back corner cover by turning the fastener one quarter turn anti-clockwise and sliding the cover up to remove.



- ❑ Make sure the lamp has cooled. Disconnect the lamp at the in-line connector. Using the key provided loosen the three locating screws, rotate lamp assembly anti-clockwise and lift lamp out.

When fitting the Deuterium lamp avoid handling the silica envelope. Finger marks become burnt on and cannot be removed after the lamp is switched on. This can affect the light output characteristics. Handle only the base of the lamp or the mounting plate. If the silica envelope becomes contaminated, clean with a powerful degreasing solvent such as absolute alcohol before the lamp is switched on.

- ❑ Take the new lamp, identify the notch in the mounting plate. Locate the lamp such that the notch points towards the lamp change mirror. Tighten locating screws down with the key provided.
- ❑ Re-connect the new lamp at the in-line connector.
- ❑ Refit the rear cover.
- ❑ Reconnect the spectrophotometer to the mains supply and switch on. Allow half an hour for warm up time.
- ❑ Lamp hours must be reset by the controlling software.

Fault Finding Guide

Problem	Symptom	Possible Cause
Instrument dead	The fans are not running	1. Ensure the mains lead is firmly pressed home. Some leads are a very tight fit in the three pin IEC connector on the rear of the instrument. 2. If a switched outlet is being used, ensure it is on. 3. Check the fuse in the plug. 4. Try another mains lead. 5. Try another mains outlet. 6. Ensure the power switch on the instrument has been fully operated. 7. If all of the above are OK the power supply may have failed. Contact your local agent.
Display Blank	No text on display, a slight glow can be seen around the edges of the display in subdued lighting.	1. The contrast control is incorrectly set. Go to the HOME page, the right and left arrow keys adjust the contrast. If nothing happens it may be that error messages are being displayed. Press the CLEAR key 5 times at 10 second intervals, to clear the error list, and try again. The display contrast is affected by temperature and may need adjusting from day to day, or as the instrument warms up. 2. The instrument has been put into remote control without allowing it to initialise first. The display will return next time that the instrument is switched on. 3. An unsuccessful attempt has been made to update the software. Connect the instrument to a PC and repeat the software upgrade process.
Any performance problem, Failure to initialise or error 1053	No light can be seen from the ventilation slots in the lamphouse cover.	1. The tungsten lamp has failed, fit a new lamp. A small number of tungsten lamps do fail very rapidly. If this happens fit a new lamp and contact your agent for a free replacement. It is likely that the spare lamp shipped with the instrument will be from the same batch as the one in the instrument.
Lamp energy low Error 1053, Drift at visible wavelengths	Instrument noisy in the visible region.	1. Check the tungsten lamp is correctly fitted and in good condition. The envelope should not show any signs of blackening or opacity. If in doubt replace with a new one. A small number of tungsten lamps do rapidly degrade. If this happens fit a new lamp and contact your agent for a free replacement.

Lamp energy low. Error 1053. Noisy signal.	Cell changer partially blocking the beam.	1. If the carousel is fitted after using another cell holder, go to the Cell Changer page and key "Initialise". 2. Make sure the carousel is not jamming or being fouled on tubing. 3. Make sure there are no cells in the beam.
Fails to initialise.	Error 3093	1. Check that the sample compartment lid is correctly shut. 2. Check that the accessory panel, found at the left hand side of the sample compartment, is in place. 3. Position the instrument so that it is not directly in strong sunlight. 4. If using a water circulator, ensure that black water tubing is used.
Deuterium lamp energy low.	Lamp energy is indicated as low but performance seems OK.	1. Lamp energy was measured with a cell in the beam. Remove all cells and re-measure the lamp energy.
Deuterium Lamp energy low.	Performance is poor in the UV region.	1. Plastic cells that do not transmit in the UV are being used. 2. The deuterium lamp may need replacing.
Fails to initialise.	Error 3027	1. Check that the beams are clear and retry. 2. Record all the error messages 3027 is a general failure message, it is usually preceded by more specific error codes. 3. Check that the tungsten lamp is working. 4. Check that the cell programmer is not blocking the beam. 5. If the problem persists insert a blank formatted disk into the disk drive. Switch the instrument on whilst holding down the RUN key. Debug data will be sent to the disk. Email the file to customer support for further help.

Connecting BioMate 5 to a PC

Terminal programmes.

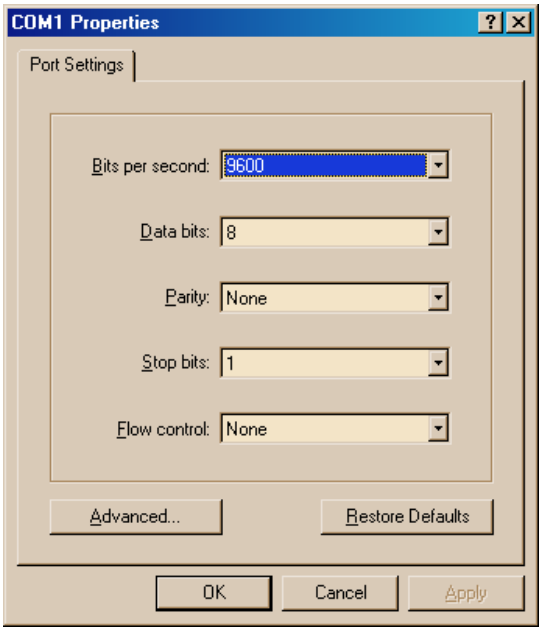
You will need software that allows you to write to and read from the computer's serial port. The communications parameters are:

Baud rate 9600
Data bits 8
Stop bits 1
No parity
Flow control off.
Local Echo on

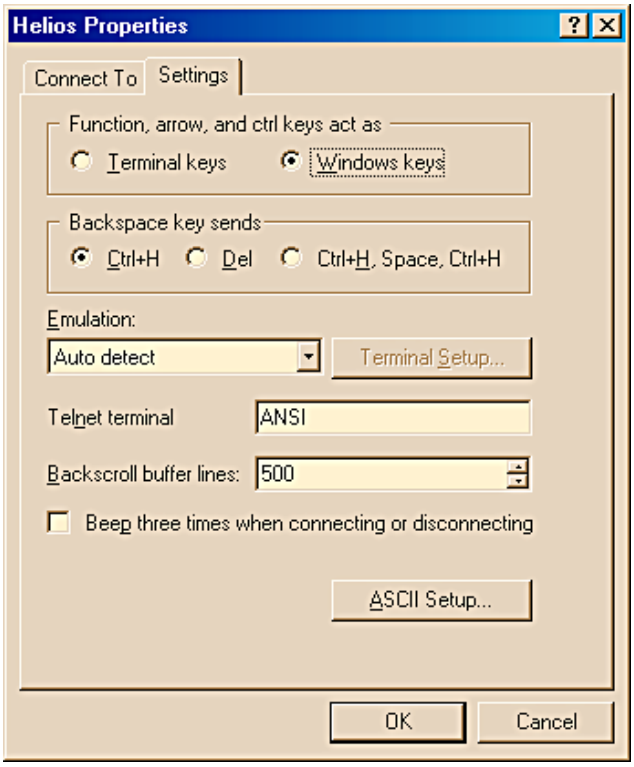
HyperTerminal

You can also use HyperTerminal that comes with Windows 95. To establish a connection, start HyperTerminal and select "New Connection" from the file menu. In the dialogue that appears, type in BioMate for the name and choose an icon. Key OK. In the next dialogue box select "Direct to COM1" and key OK.

Fill in the COM 1 properties dialogue box as shown below.



Then from the FILE menu select PROPERTIES and then click on the SETTINGS tab. Fill in the dialogue box as shown below. Click on OK.



Connecting BioMate 5 to a PC

1) Use a null modem cable (part number 4013 172 82111) to connect the RS232C port of BioMate 5 to a free COM port on the PC.

   Here is the pin out data for the RS232 Cable

Pin		Pin
9	to	9
2		3
3		2
4		8
8		4
6		1 and 7
1 and 7		6
5		5
Earth		Earth

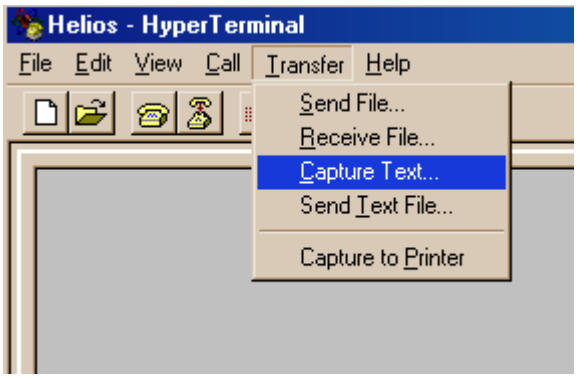
Switch on the PC and set up a terminal programme as described above.

Collecting Data

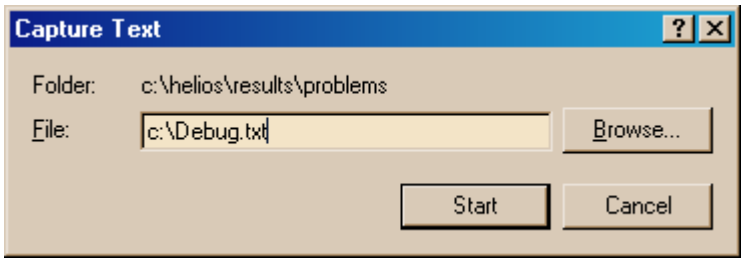
Once you have established control of the instrument and switched on the debug software you will need to collect the data that is returned and save it to file. This can be done by several methods, the next section details one of them.

Using Hyperterminal to collect data

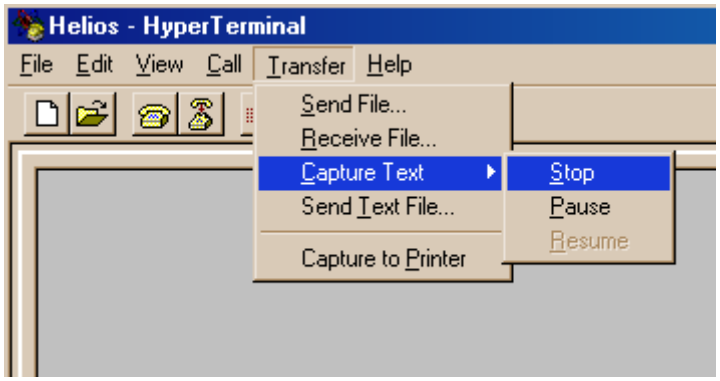
1) From the menu bar select TRANSFERS and then CAPTURE TEXT.



2) The CAPTURE TEXT dialogue box appears. Type in a path and file name then key START.



3) Once the instrument has stopped sending data, from the menu bar Select TRANSFER then CAPTURE TEXT then key STOP to terminate the transfer and save the file.



BIOMATE 5 TEST PARAMETERS

The following table lists alphabetically all the parameters used for the BioMate Tests. The list includes a brief description of each parameter, the applicable range and the initial default values. Use this list as a reference when setting up tests.

PARAMETER	DESCRIPTION	INITIAL DEFAULT VALUES	RANGE
%Formamide	Percentage of formamide contained in the sample	50	1-100 Integer
%GC	Percentage of GC pairs contained in the sample	empty; not an entry	NA
%Mismatched	Percentage of mismatched bases in the sample	0	1-100 Integer
Auto Print	Turns automatic printout on or off	Off	On↔Off
Base Sequence	Sequence of bases contained in the sample	empty field, unless sequence entered previously	40 characters max.
Cation Molarity	Molarity of cation (Na) contained in the sample	0.050	0.001-9999
Curve Fit	Type of Line fit calculation	Std Curve: Linear Bradford-Standard: Quadratic Bradford-micro: Quadratic Lowry-Standard: Quadratic Lowry-micro: Quadratic BCA-Standard: Quadratic BCA-micro: Quadratic Biuret: Linear Through Zero	Linear Linear Through Zero Quadratic Quadratic Through Zero
Date Standards Measured	Date when standards were last measured with this instrument	------	
Diluent Volume	Volume of diluent added prior to measurement	0	0-999 Integer
Dilution Multiplier	Factor used to correct for sample dilution	1.00	1.00-99999 x.xx xx.xx xxx.x xxxx xxxxx
Display Protein	Indicates whether results should appear as units of protein concentration	On	On↔Off
DNA ε(260)	Extinction coefficient	empty; not an entry	NA
DNA Mol. Wt.	Molecular weight of DNA contained in sample	empty; not an entry	NA

PARAMETER	DESCRIPTION	INITIAL DEFAULT VALUES	RANGE
Factor	See individual calculations for usage	DNA (260/280), DNA with Scan (260/280): DNA Factor @260: 62.9 DNA Factor @280: 36.0 Protein Factor @260: 757.3 Protein Factor @280: 1552 DNA (260/230), DNA with Scan (260/230): DNA Factor @260: 49.1 DNA Factor @230: 3.48 Protein Factor @260: 75.8 Protein Factor @230: 183 dsDNA: 50 ssDNA, ssRNA: 40 Direct UV-Oligos : 33 Direct UV (280): 1 Direct UV (205): 31 Oligo calculator: blank if no base sequence entered; calc value if base sequence entered Warburg-Christian: 1.55 @ 280; 0.76 @ 260	-0.001 to -99999; 0.001 to 99999 x.xxx xx.xx xxx.x xxxx xxxxx
ID#	Numeric Identifier – autoincrements during test until reset or test is exited	1	0=OFF 1-999 Integer
Low/High Limits	Lowest & highest acceptable results, outside of which the result is flagged as 'Low' or 'High'	-9999/9999	±9999
Number of Bases	Number of bases contained in sample	empty; not an entry	NA
Number of Samples	Number of samples to be measure in the whole test	1	1-999 Integer
Number of Standards	Number of standards to be measured for calibration curve	Bradford, Lowry, BCA, Biuret: 6	1-20 Integer
Ref. Wavelength	Internal Reference wavelength; for each reported measurement, measures analytical wavelength & reference wavelength. Reported measurement = abs @ analytical WL – abs @ Reference WL	DNA: 320	190-1100
Ref. Wavelength Correction	Turns internal zeroing on or off	Off	On↔Off
Sample Positioner	Manual = moved by buttons Auto 6 + Ref = auto moved –Ref, 2,3,4,5,6,7 Auto 7 = auto moved – 1,2,3,4,5,6,7	Auto 6 +Ref if 7 Cell Changer fitted Not displayed if Single Cell Holder fitted	Auto 7 / Auto 6 + Ref. / Manual 7 for 7 Cell Changer; no choice for Single Cell Holder
Sample Volume	Total volume of sample	1	1-999 Integer
Scan Start	Start wavelength for scan	225.0nm	190.0 – 1100.0
Scan Stop	Final wavelength for scan	325.0nm	190.0 – 1100.0
Standard Concentrations	Concentration of standards used to generate standard curve for the test	Bradford-Std: 0, 200, 400, 600, 800, 1000 Bradford-micro: 0, 20, 40, 60, 80, 100 Lowry-Std: 0, 100, 200, 500, 1000, 2000 Lowry-micro: 0, 20, 50, 100, 200, 500 BCA-Std: 0, 0.2, 0.4, 0.6, 0.8, 1.0 BCA-micro: 0, 0.5, 1, 2, 5, 10 Biuret: 0, 2, 4, 6, 8, 10	0.000-9999

PARAMETER	DESCRIPTION	INITIAL DEFAULT VALUES	RANGE
Statistics	Turns statistics function on or off; if ON, calculates average and Std Dev of results;	Off	On↔Off
Test Name	Defined by user to identify stored tests	DNA (260/280) DNA (260/230) DNA WITH SCAN dsDNA ssDNA, RNA OLIGOS (FACTOR) OLIGOS (CALC) BRADFORD-STANDARD BRADFORD-MICRO LOWRY-STANDARD LOWRY-MICRO BCA-STANDARD BCA-MICRO BIURET DIRECT UV (280) DIRECT UV (205) WARBURG-CHRISTIAN CELL GROWTH	up to 19 characters
Tm values	Predicted melting point temperatures	empty; not an entry	NA
Units	Labels concentration results	DNA Ratio: μg/ml for DNA & Protein DNA Scan: μg/ml for DNA & Protein dsDNA: μg/ml ssDNA & RNA: μg/ml Oligos: μg/ml Bradford Protein: μg/ml Lowry Protein: μg/ml BCA-Standard Protein: mg/ml BCA-micro: μg/ml Biuret Protein: mg/ml Direct UV Protein: mg/ml Warburg-Christian: mg/ml	Up to 9 characters
Wavelength values	Values for the analytical wavelengths	DNA: 260, 280; 260, 230 dsDNA, ssDNA, RNA: 260 DNA scan: 225, 325 Oligos (entered factor): 260 Oligos (calc factor): 260 Bradford-Standard & -micro: 595 Lowry-Standard: 550 Lowry-micro: 750 BCA-Standard & -micro: 562 Biuret: 540 Direct UV: 280 Direct UV: 205 Warburg-Christian: 260, 280 Cell Growth: 600	190.0-1100.0nm

CALCULATIONS FOR BIOMATE 5 TESTS

Test Name	Test Types	Calculation (s)	Default Parameters	Displayed Units
DNA/Protein concentration and DNA Purity (260, 280)	Absorbance Difference + Absorbance Ratio	*Dilution Factor (D_f)* = $\frac{\text{diluent vol + sample volume}}{\text{sample volume}}$ *DNA concentration* = $[(A_1 - A_{ref})f_1 - (A_2 - A_{ref})f_2]D_f$ *Protein concentration* = $[(A_2 - A_{ref})f_3 - (A_1 - A_{ref})f_4]\ D_f$ *Ratio* = $\frac{A_1 - A_{ref}}{A_2 - A_{ref}}$	A_1 = 260nm A_2 = 280nm A_{ref} = 320nm (optional) f_1 = 62.9 f_2 = 36.0 f_3 = 1552 f_4 = 757.3 dil.vol. = 0 smp.vol = 1	DNA: µg/ml Protein: µg/ml Ratio: no units
DNA/Protein concentration and DNA Purity (260, 230)	Absorbance Difference + Absorbance Ratio	*Dilution Factor (D_f)* = $\frac{\text{diluent vol + sample volume}}{\text{sample volume}}$ *DNA concentration* = $[(A_1 - A_{ref})f_1 - (A_2 - A_{ref})f_2]\ D_f$ *Protein concentration* = $[(A_2 - A_{ref})f_3 - (A_1 - A_{ref})f_4]\ D_f$ *Ratio* = $\frac{A_1 - A_{ref}}{A_2 - A_{ref}}$	A_1 = 260nm A_2 = 230nm A_{ref} = 320nm (optional) f_1 = 49.1 f_2 = 3.48 f_3 = 183 f_4 = 75.8 dil vol. = 0 smp.vol = 1	DNA: µg/ml Protein: µg/ml Ratio: No units
DNA/Protein concentration and DNA Purity (260, 280) with SCAN	Scan – Absorbance	None	Start wavelength = 230nm Stop wavelength = 330nm	None
	Absorbance Difference + Absorbance Ratio + Scan	*Dilution Factor (D_f)* = $\frac{\text{diluent vol + sample vol.}}{\text{sample volume}}$ *DNA concentration* = $[(A_1 - A_{ref})f_1 - (A_2 - A_{ref})f_2]\ ]\ D_f$ *Protein concentration* = $[(A_2 - A_{ref})f_3 - (A_1 - A_{ref})f_4]\ ]\ D_f$ *Ratio* = $\frac{A_1 - A_{ref}}{A_2 - A_{ref}}$	A_1 = 260nm A_2 = 280nm A_{ref} = 320nm (optional) f_1 = 62.9 f_2 = 36.0 f_3 = 1552 f_4 = 757.3 dil.vol. = 0 smp.vo. = 0	DNA: µg/ml Protein: µg/ml
DNA/Protein concentration and DNA Purity (260, 230) with SCAN	Scan – Absorbance	None	Start wavelength = 230nm Stop wavelength = 330nm	None
	Absorbance Difference + Absorbance Ratio + Scan	*Dilution Factor (D_f)* = $\frac{\text{diluent vol + sample vol.}}{\text{sample volume}}$ *DNA concentration* = $[(A_1 - A_{ref})f_1 - (A_2 - A_{ref})f_2]\ ]\ D_f$ *Protein concentration* = $[(A_2 - A_{ref})f_3 - (A_1 - A_{ref})f_4]\ ]\ D_f$ *Ratio* = $\frac{A_1 - A_{ref}}{A_2 - A_{ref}}$	A_1 = 260nm A_2 = 230nm A_{ref} = 320nm (optional) f_1 = 49.1 f_2 = 3.48 f_3 = 183 f_4 = 75.8 dil.vol. = 0 smp.vol. = 0	DNA: µg/ml Protein: µg/ml
Direct UV – dsDNA	Factor	*Conc.* = F x A_{260}	260nm $Factor_{dsDNA}$ = 50	µg/ml
Direct UV – ssDNA or RNA	Factor	*Conc.* = F x A_{260}	260nm $Factor_{ssDNA\ or\ ssRNA}$ = 40	µg/ml
Direct UV – oligos (w/base calculator)	Factor	*Conc.* = F x A_{260} F = factor calculated by Oligo Calculator	260nm	µg/ml
Direct UV - oligos	Factor	*Conc.* = F x A_{260}	260nm $Factor_{oligos}$ = 33	µg/ml
Bradford – standard	Standard Curve	Second order	595nm Standard concentrations of 0, 200, 400, 600, 800, 1000	100 - 1000µg/ml
Bradford – micro	Standard Curve	Second order	595nm Standard concentrations of 0, 20, 40, 60, 80, 100	10 - 100µg/ml
Lowry – standard	Standard Curve	Second order	550nm Standard concentrations of 0, 100, 200, 500, 1000, 2000	100 - 2000µg/ml
Lowry – micro	Standard curve	Second order	750nm Standard concentrations of 0, 20, 50, 100, 200, 500	10 - 500µg/ml
Bicinchoninic Acid (BCA) – standard	Standard Curve	Second order	562nm Standard concentrations of 0, 0.2, 0.4, 0.6, 0.8, 1	0.1 – 1mg/ml
Bicinchoninic Acid (BCA) – micro	Standard Curve	Second order	562nm Standard concentrations of 0, 0.5, 1, 2, 5, 10	0.5 - 10µg/ml
Biuret	Standard Curve	First order through zero	540nm Standard concentrations of 0, 2, 4, 6, 8, 10	0 – 10mg/ml
Direct UV (280)	Factor	*Conc.* = F x A_{280}	280nm $Factor_{280}$ = 1	mg/ml
Direct UV (205)	Factor	*Conc.* = F x A_{205}	205nm $Factor_{205}$ = 31	mg/ml
Warburg-Christian	Absorbance difference	*Dilution Factor (D_f)* = $\frac{\text{diluent vol + sample vol.}}{\text{sample volume}}$ *Protein Concentration* = $[A_1 f_1 - A_2.f_2]\ D_f$	A_1 = 280nm A_2 = 260nm f_1 = 1.55 f_2 = 0.76	mg/ml
Cell growth	Absorbance	None	600nm	Abs

BIOMATE OLIGO CALCULATOR

Calculation Name	Entry Parameters	Formula	Displayed Units
# of bases	Repetitive sequence of A, T, G and C	Count of total # of bases entered	Length = # of bases
%GC content	Use ATGC sequence entered above	%GC = $\frac{\#\text{ of (G + C) bases}}{\text{total \# of ATGC}} \times 100$	Percentage
Molecular weight	# units A, # units T, # units G, # units C	MW = (312.2 x A) + (328.2 x T) + (288.2 x G) + (303.2 x C) - 61	Molecular weight = x daltons/M
Absorptivity	# units A, # units T, # units G, # units C	ε_{260} = (16,000 x A) + (9,600 x T) + (12,000 x G) + (7,000 x C)	Extinction coefficient = $M^{-1}cm^{-1}$
Factor	N/A	$\frac{\text{Molecular Weight} \times 10^3}{\text{Extinction Coefficient}}$	µg/mL
Calculation of T_m: Oligos up to 40-mers in length	# units A, # units T, # units G, # units C	$T_m = 2(A + T) + 4(G + C)$	°C
Calculation of T_m: DNA-DNA hybrids	▪ # units A, # units T, # units G, # units C ▪ M = molarity of Na ▪ %GC = percentage of G and C ▪ %form = %formamide in the solution ▪ L = # of base pairs ▪ P = % mismatched	Tm = 81.5+16.6log10((M)/(1+0.7(M))+0.41(%GC)-500/L-P-0.63(%form)	°C
Calculation of T_m: DNA-RNA hybrids	▪ # units A, # units T, # units G, # units C ▪ M = molarity of Na ▪ %GC = percentage of G and C ▪ %form = %formamide in the solution ▪ L = # of base pairs ▪ P = % mismatched	Tm = 67+16.6log10((M)/(1+0.7(M))+0.8(%GC)-500/L-P-0.5(%form)	°C
Calculation of T_m: RNA-RNA hybrids	▪ # units A, # units T, # units G, # units C ▪ M = molarity of Na ▪ %GC = percentage of G and C ▪ %form = %formamide in the solution ▪ L = # of base pairs ▪ P = % mismatched	Tm = 78+16.6log10((M)/(1+0.7(M))+0.7(%GC)-500/L-P-0.35(%form)	°C